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(54) Title: NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

(57) Abstract: The invention provides nucleic acids containing single-nucleotide polymorphisms identified for transcribed human sequences, as well as methods of using the nucleic acids.

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# NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

## BACKGROUND OF THE INVENTION

Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. The approach is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in identity and paternity analysis, and in genetic mapping studies.

One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPS can create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is an alteration in the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences typically include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA.

SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at which one allele bears a gap with respect to a single nucleotide in another allele. Some SNPs occur within, or near genes. One such class includes SNPs falling within regions of genes

encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, *e.g.*, genetic disease. Examples of genes in which a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the genome. The frequency and uniformity of SNPs means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest.

#### SUMMARY OF THE INVENTION

The invention is based in part on the discovery of novel single nucleotide polymorphisms (SNPs) in regions of human DNA.

Accordingly, in one aspect, the invention provides an isolated polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7024) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS: 1-7024), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The polynucleotide can be, *e.g.*, DNA or RNA, and can be between about 10 and about 100 nucleotides, *e.g.* 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

In some embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, *e.g.*, the polymorphic site includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of

the polymorphic sequence, *e.g.*, the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to an ATPase associated protein, a cadherin, or any of the other proteins identified in Table 1, column 10.

In another aspect, the invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7024), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7024), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, *e.g.*, (a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7024), wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence; (b) a nucleotide sequence that is a fragment of any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7024), wherein the polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.



The invention also provides a method of detecting a polymorphic site in a nucleic acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

In some embodiments, the polymorphic sequence identified by the oligonucleotide is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated polypeptide related to an ATPase associated protein, cadherin, or any of the other protein families identified in Table 1, column 10.

In another aspect, the method includes determining if a sequence polymorphism is the present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In a further aspect, the invention provides a method of determining the relatedness of a first and second nucleic acid. The method includes providing a first nucleic acid and a second

nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids to the nucleic acid indicates the first and second subjects are related.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from the child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences SEQ ID NOS:1-7024, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, *e.g.*, related to one of the protein families disclosed herein. For example, polypeptide can be related to an ATPase associated protein, cadherin, or any of the other proteins provided in Table 1, column 10.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

In some embodiments, the polypeptide encoded by the polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7024, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen complexes. The antibody-antigen complexes are then detected. The presence of the complexes indicates the presence of the polypeptide.

The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism

in a subject, *e.g.*, a human, non-human primate, cat, dog, rat, mouse, cow, pig, goat, or rabbit. The method includes providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively different polypeptides can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene. Finally, aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

The therapeutic agent can include, *e.g.*, second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence comprises a polymorphic sequence which includes nucleotide listed in Table 1, column 5 for the polymorphic sequence.

Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7024, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7024, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for the polymorphic sequence.

In another aspect, the invention provides an oligonucleotide array comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed

therein. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7024); a nucleotide sequence that is a fragment of any of the nucleotide sequences, provided that the fragment includes a polymorphic site in the polymorphic sequence; a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7024); or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described nucleic acids. The kit can include, e.g., a polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, e.g., a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7024) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS:1-7024), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence. The invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7024), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7024), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention

belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

### DETAILED DESCRIPTION OF THE INVENTION

The present invention provides 3,404 distinct polymorphic sites (i.e., human cSNP's) based on genes that have not yet been previously identified. They are described in the Table included with this application for patent. The instant application presents only polymorphisms in nucleic acid sequences that have not previously been identified. For this reason, both nucleotide sequences for a reference-polymorphic pair are presented in the instant application. Since neither sequence was known prior to this invention, the choice of designating one sequence of the cognate pair as a "reference" sequence and the second cognate of the pair as a "polymorphic" sequence is arbitrary.

The SNPs are shown in Table 1 and the Sequence Listing. Both provide a summary of the polymorphic sequences disclosed herein. In the Table, a "SNP" is a polymorphic site embedded in a polymorphic sequence. The polymorphic site is occupied by a single nucleotide, which is the position of nucleotide variation between the wild type and polymorphic allelic sequences. The site is usually preceded by and followed by relatively highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations). Thus, a polymorphic sequence can include one or more of the following sequences: (1) a sequence having the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence; or (2) a sequence having a nucleotide other than the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence. An example of the latter sequence is a polymorphic sequence having the nucleotide denoted in Table 1, column 6 at the polymorphic site in the polymorphic sequence.

Nucleotide sequences for a referenced-polymorphic pair are presented in Table 1. Each cSNP entry provides information concerning the wild type nucleotide sequence as well as the corresponding sequence that includes the SNP at the polymorphic site. Since the wild type sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele; its SEQ ID NO: is also cross referenced in the Table 1. A reference to the SEQ ID NO: giving the translated amino acid sequence is also given if appropriate. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

"SEQ ID" provides the cross-references to the two nucleotide SEQ ID NOs: for the cognate pair, which are numbered consecutively, and, as explained below, amino acid SEQ ID NOs: as well, in the Sequence Listing of the application. Conversely, each sequence entry in the Sequence Listing also includes a cross-reference to the CuraGen sequence ID, under the label "CuraGen sequence ID". The first pair of SEQ ID NOs: given in the first column of each row of the Table are the SEQ ID NOs: identifying the nucleic acid sequences for the polymorphisms. If a polymorphism carries an entry for the amino acid portion of the row, a third SEQ ID NO: appears in parentheses in the column "Amino acid before" (see below) for the reference amino acid sequence, and a fourth SEQ ID NO: appears in parentheses in the column "Amino acid after" (see below) for the polymorphic amino acid sequence. The latter SEQ ID NOs: refer to amino acid sequences giving the cognate reference and polymorphic amino acid sequences that are the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one pair SEQ ID NOs: is provided, in the first column.

"Base pos. of SNP" gives the numerical position of the nucleotide in the nucleic acid at which the cSNP is found, as identified in this invention.

"Polymorphic sequence" provides a 51-base sequence with the polymorphic site at the 26<sup>th</sup> base in the sequence, as well as 25 bases from the reference sequence on the 5' side and the 3' side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a "slash (/)"; and third, the polymorphic nucleotide. In certain cases the polymorphism is an insertion or a deletion. In that case, the position which is "unfilled" (i.e., the reference or the polymorphic position) is indicated by the word "gap".

“Base before” provides the nucleotide present in the reference sequence at the position at which the polymorphism is found.

“Base after” provides the altered nucleotide at the position of the polymorphism.

“Amino acid before” provides the amino acid in the reference protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses for the translated reference amino acid sequence if the polymorphism occurs in a coding region.

“Amino acid after” provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses for the translated polymorphic amino acid sequence if the polymorphism occurs in a coding region.

“Type of change” provides information on the nature of the polymorphism.

“SILENT-NONCODING” is used if the polymorphism occurs in a noncoding region of a nucleic acid.

“SILENT-CODING” is used if the polymorphism occurs in a coding region of a nucleic acid and results in no change of amino acid in the translated polymorphic protein.

“CONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are:

Aliphatic: Gly, Ala, Val, Leu, Ile;

Aromatic: Phe, Tyr, Trp;

Sulfur-containing: Cys, Met;

Aliphatic OH: Ser, Thr;

Basic: Lys, Arg, His;

Acidic: Asp, Glu, Asn, Gln;



Pro falls in none of the other classes; and

End defines a termination codon.

“NONCONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

“FRAMESHIFT” relates to an insertion or a deletion. If the frameshift occurs in a coding region, the Table provides the translation of the frameshifted codons 3' to the polymorphic site.

“Protein classification of CuraGen gene” provides a generic class into which the protein is classified. During the course of the work leading to the filing of the four applications identified above, approximately 100 classes of proteins were identified. They are described further below.

“Name of protein identified following a BLASTX analysis of the CuraGen sequence” provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely. (The next paragraph explains how a sequence was determined to be “novel”).

“Similarity (pvalue) following a BLASTX analysis” provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of  $pvalue > 1 \times 10^{-50}$  (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel.

“Map location” provides any information available at the time of filing related to localization of a gene on a chromosome.

The polymorphisms are arranged in the Table in the following order.

SEQ ID NOs: 1-6592, in consecutive pairs, are SNPs that are silent.

SEQ ID NOs: 6593-6648, in consecutive pairs, are SNPs that lead to conservative amino acid changes.

SEQ ID NOs: 6649-7024, in consecutive pairs, are SNPs that lead to nonconservative amino acid changes.

SEQ ID NOs: 6809-6864, in consecutive pairs, are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes between the reference and the polymorphic sequences. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 44335-44850, as described in U.S.S.N. 60/168,138, filed November 30, 1999. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

SEQ ID NOs: 6865-7024, in consecutive pairs, are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative amino acid changes between the reference and the polymorphic sequences. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 44851-46464, as described in U.S.S.N. 60/168,138, filed November 30, 1999. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

#### IDENTIFICATION OF INDIVIDUALS CARRYING SNPs

Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by *e.g.*, PCR. See generally PCR Technology: Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992);

PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, i.e., a "polymorphic protein" containing an altered amino acid at the site of translation of the nucleotide polymorphism. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The phrase "substantially purified" or "isolated" when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or preferably, essentially none, of other cellular components with which it is naturally associated. Thus, the phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as gel electrophoresis or high performance liquid chromatography. Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace

Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art. A "nucleic acid" is a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term "nucleic acids", as used herein, refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide bases read from the 5' end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence. "Nucleic acid probes" may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl. Acids Res. 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. USA, 86:6230-6234 (1969)) or oligonucleotide arrays (Maskos and Southern Nucl. Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995)), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. Proc. Natl. Acad. Sci. U.S.A. 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. w Sci. U.S.A., 8Z4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific

primer extension (Syvanen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. &&I Acids 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-193 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., Nucl. Acids Res, 21:5332-5356 (1993); Thiede et al., Nucl. Acids Res. 24:983-984 (1996)).

“Specific hybridization” or “selective hybridization” refers to the binding, or duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). “Stringent conditions” are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The T<sub>m</sub> is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridization.

“Complementary” or “target” nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe’s length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or Current Protocols in Molecular Biology, F. Ausubel *et al.*, ed., Greene Publishing and Wiley-Interscience, New York (1987).

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A "polymorphic" marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative, variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.

As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of a complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation. Oligonucleotide probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the

template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett 22:1859-1862 (1981) and the triester method provided by Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., Nucleic Acids Res. 12:61596168 (1984). Purification of oligonucleotides may be carried out by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand using a DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The sequence of the synthetic oligonucleotide or of any nucleic acid fragment can be obtained using either the dideoxy chain termination method or the Maxam-Gilbert method (see Sambrook et al. Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al."; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, (Acad. Press, New York). Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the SNP-

containing nucleotide sequences of the invention, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire SNP coding strand, or to only a portion thereof.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to the entire coding region of an mRNA, but more preferably as embodied herein, it is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more preferably between about 15 and 30 in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-



2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The

antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman *Adv. Appl. Math.* 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson and Lipman *Proc. Natl. Acad. Sci. U.S.A.* 852444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described generally in Sambrook *et al.*, The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based

on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assays of genomic DNA, virtually any biological convenient tissue sample can be used. Suitable samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. Genomic DNA is typically amplified before analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNase.

#### **DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE**

The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7, 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in published PCT application WO 95/11995. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on a target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base

sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach, leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are within a 50,000 bp region in the human genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic

loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a match of suspect and crime scene sample would occur by chance.

$p(ID)$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism are (see WO 95/12607):

$$\text{Homozygote: } p(AA)=x^2$$

$$\text{Homozygote: } p(BB)=y^2=(1-x)^2$$

$$\text{Single Heterozygote: } p(AB)=p(BA)=xy=x(1-x)$$

$$\text{Both Heterozygotes: } p(AB+BA)=2xy=2x(1-x)$$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID)=(x^2)^2+(2xy)^2+(y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(ID)$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID)=x^4+(2xy)^2+(2yz)^2+(2xz)^2+z^4+y^4$$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(ID)$  and  $p(exc)$ .

The cumulative probability of identity ( $cum\ p(ID)$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$cum\ p(ID)=p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$cum\ p(nonID)=1-cum\ p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$$p(exc)=xy(1-xy)$$

where  $x$  and  $y$  are the population frequencies of alleles A and B of a diallelic polymorphic site.

(At a triallelic site  $p(exc) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where  $x$ ,  $y$  and  $z$  and the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

$$p(non-exc) = 1 - p(exc)$$

The cumulative probability of non-exclusion (representing the value obtained when  $n$  loci are used) is thus:

$$cum\ p(non-exc) = p(non-exc1)p(non-exc2)p(non-exc3) \dots p(non-excn)$$

The cumulative probability of exclusion for  $n$  loci (representing the probability that a random male will be excluded) is:

$$cum\ p(exc) = 1 - cum\ p(non-exc).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus



erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic marker sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $RF$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $RF$ ), ranging

from  $RF=0.0$  (coincident loci) to  $RF=0.50$  (unlinked). Thus, the likelihood at a given value of  $RF$  is: probability of data if loci linked at  $RF$  to probability of data if loci unlinked. The computed likelihood is usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of  $RF$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $RF$  at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $RF$ ) than the possibility that the two loci are unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292. The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

The invention further provides methods for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular

pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmacogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the cause of a pathological condition, method of treating such a condition includes administering to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

A subject suspected of suffering from a pathology ascribable to a polymorphic protein that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by administering a normal or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid may be administered include incorporating the wild-type gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample

drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening

cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. *Gene* 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, *Science* 196:180-182 (1977). Colony hybridization is carried out as generally described in M. Grunstein et al. *Proc. Natl. Acad. Sci. USA*. 72:3961-3965 (1975). DNA of interest is identified in either cDNA or genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be used in a variety of protocols to isolate cDNAs encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either

prokaryotes or eukaryotes. Typical expression vectors contain initiation sequences, transcription and translation terminators, and promoters useful for regulation of the expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacterial. 158:1018-1024 (1984) and the leftward promoter of phage lambda as described by A, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the

invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., *Gene* 8:17-24 (1979); Broach, et al., *Gene* 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glusulase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, *Nature* (London) 275:104-109 (1978); and Hinnen, A., et al., *Proc. Natl. Acad. Sci. USA*, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., *J. Bact.* 153:163-168 (1983)) cells and applying standard protein isolation techniques to the lysates.

The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen et al. *Immunol. Rev.* 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.



Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider J. Embryol. Exp. Morphol., 27:353-365 (1987)). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, J. et al., J. Virol. 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the gene encoding the protein is expressed

by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated nucleotide sequences. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida* or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac© kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed." The protein of the invention may

be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.

The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may be purified to substantial purity by standard techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl® or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New

England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$  and  $F_{(ab)2}$  fragments, and an  $F_{ab}$  expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically immunoreactive with", an antibody when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, a Laboratory Manual*, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

Polyclonal and/or monoclonal antibodies that immunospecifically bind to polymorphic gene products but not to the corresponding prototypical or "wild-type" gene

products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that binds the polymorphic protein using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the surface of the protein, *e.g.*, hydrophilic regions.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography, to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that originates from the clone of a singly hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polymorphic protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a polymorphic protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of F<sub>ab</sub> expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F<sub>ab</sub> fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotype to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (i) an F<sub>(ab)<sup>2</sup></sub> fragment produced by pepsin digestion of an antibody molecule; (ii) an F<sub>ab</sub> fragment generated by reducing the disulfide bridges of an F<sub>(ab)<sup>2</sup></sub> fragment; (iii) an F<sub>ab</sub> fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F<sub>v</sub> fragments.

Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by

recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988) *J Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060.

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable

substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

#### EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that unique compositions and methods of use thereof in SNPs in known genes have been described. Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims which follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims.



**WHAT IS CLAIMED IS:**

1. An isolated polynucleotide selected from the group consisting of:
  - a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024;
  - b) a fragment of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
  - c) a complementary nucleotide sequence comprising a sequence complementary to one or more of said polymorphic sequences selected from the group consisting of SEQ ID NOS:1-7024; and
  - d) a fragment of said complementary nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.
2. The polynucleotide of claim 1, wherein said polynucleotide sequence is DNA.
3. The polynucleotide of claim 1, wherein said polynucleotide sequence is RNA.
4. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 100 nucleotides in length.
5. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 90 nucleotides in length.
6. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 75 nucleotides in length.
7. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and about 50 bases in length.
8. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and about 40 bases in length.
9. The polynucleotide of claim 1, wherein said polynucleotide is between about 15 and about 30 bases in length.

10. The polynucleotide of claim 1, wherein said polymorphic site includes a nucleotide other than the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
11. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of said polymorphic sequence.
12. The polynucleotide of claim 1, wherein said polymorphic site includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
13. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes the complement of the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
14. An isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is selected from the group consisting of:
  - a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024 provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence;
  - b) a nucleotide sequence that is a fragment of said polymorphic sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
  - c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024, provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
  - d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

15. The oligonucleotide of claim 14, wherein the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide selected from the group consisting of:
- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024, wherein said polymorphic sequence includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence;
  - b) a nucleotide sequence that is a fragment of any of said nucleotide sequences;
  - c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024, wherein said polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and
  - d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.
16. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 51 bases in length.
17. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 40 bases in length.
18. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 15 and about 30 bases in length.
19. A method of detecting a polymorphic site in a nucleic acid, the method comprising:
- a) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
  - b) determining whether said nucleic acid and said oligonucleotide hybridize;

whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphic site in said nucleic acid.

20. The method of claim 19, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.
21. The method of claim 19, wherein said oligonucleotide is between about 10 and about 51 bases in length.
22. The method of claim 19, wherein said oligonucleotide is between about 10 and about 40 bases in length.
23. A method of detecting the presence of a sequence polymorphism in a subject, the method comprising:
  - a) providing a nucleic acid from said subject;
  - b) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
  - c) determining whether said nucleic acid and said oligonucleotide hybridize; whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphism in said subject.
24. A method of determining the relatedness of a first and second nucleic acid, the method comprising:
  - a) providing a first nucleic acid and a second nucleic acid;
  - b) contacting said first nucleic acid and said second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7024, or its complement, provided that

the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;

- c) determining whether said first nucleic acid and said second nucleic acid hybridize to said oligonucleotide; and
  - d) comparing hybridization of said first and second nucleic acids to said oligonucleotide, wherein hybridization of first and second nucleic acids to said nucleic acid indicates the first and second subjects are related.
25. The method of claim 24, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.
26. The method of claim 24, wherein the oligonucleotide is between about 10 and about 51 bases in length.
27. The method of claim 24, wherein the oligonucleotide is between about 10 and about 40 bases in length.
28. The method of claim 24, wherein the oligonucleotide is between about 15 and about 30 bases in length.
29. An isolated polypeptide comprising a polymorphic site at one or more amino acid residues, wherein the protein is encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7024, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

30. The polypeptide of claim 29, wherein said polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.
31. The polypeptide of claim 29, wherein the polypeptide encoded by said polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.
32. An antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7024, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.
33. The antibody of claim 32, wherein said antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
34. The antibody of claim 32, wherein said antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
35. A method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject, the method comprising
- a) providing a protein sample from said subject;
  - b) contacting said sample with the antibody of claim 34 under conditions that allow for the formation of antibody-antigen complexes; and
  - c) detecting said antibody-antigen complexes,
- whereby the presence of said complexes indicates the presence of said polypeptide.

36. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:
- a) providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or its complement; and
  - b) administering to the subject an effective therapeutic dose of a second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele,
- thereby treating said subject.
37. The method of claim 36, wherein the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
38. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:
- a) providing a subject suffering from a pathology associated with aberrant expression of a polymorphic sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1 - 7024, or its complement; and
  - b) administering to the subject an effective therapeutic dose of a polypeptide,
- wherein said polypeptide is encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7024, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

39. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:
- a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or its complement; and
  - b) administering to the subject an effective dose of the antibody of claim 34, thereby treating said subject.
40. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:
- a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or its complement; and
  - b) administering to the subject an effective dose of an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7024, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7024, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for said polymorphic sequence, thereby treating said subject.
41. An oligonucleotide array, comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is chosen from the group consisting of:
- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024;
  - b) a nucleotide sequence that is a fragment of any of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;



- c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7024; and
  - d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.
42. The array of claim 41, wherein said array comprises about 10 oligonucleotides.
43. The array of claim 41, wherein said array comprises about 100 oligonucleotides.
44. The array of claim 41, wherein said array comprises about 1000 oligonucleotides.

## SEQUENCE LISTING

<110> Shimkets, Richard A.  
Leach, Martin D.

<120> NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND METHODS OF  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43299481

<400> 24

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50

<210> 25

<211> 51

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<223> 1 of 2 allelic variants (26 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43299481

<400> 25  
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<210> 26  
<211> 51  
<212> DNA  
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<221> misc\_feature  
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<400> 26  
caccttcaca gccacccctt tcgccgtctc ctcccatgtc gggatcttct t 51

<210> 27  
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<220>  
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<223> 1 of 2 allelic variants (28 is other entry)

<221> misc\_feature  
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<223> Accession number cg43941958

<400> 27  
ggaaatgccca cattccatag cgcagcttgc actgcacact gctatgaatt c 51

<210> 28  
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<220>  
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<223> 2 of 2 allelic variants (27 is other entry)

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<223> Accession number cg43941958

<400> 28  
ggaaatgccca cattccatag cgcagtttgc actgcacact gctatgaatt c 51

<210> 29  
<211> 51  
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<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (30 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27363108

<400> 29

gtgcaatgca gttcacacat acctggaatt tatgcagatg ttcagatata g

51

<210> 30

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (29 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27363108

<400> 30

gtgcaatgca gttcacacat acctgaaatt tatgcagatg ttcagatata g

51

<210> 31

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (32 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44921820

<400> 31

tgggtaaagg ggattctggg agttgagagc tctgccaggg tgagatgttt c

51

<210> 32

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (31 is other entry)

<221> misc\_feature  
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<223> Accession number cg44921820

<400> 32  
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51

<210> 33  
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<212> DNA  
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<223> 1 of 2 allelic variants (34 is other entry)

<221> misc\_feature  
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<223> Accession number cg43988115

<400> 33  
atgcttagat gtggtgctgt ggtgctgtgc atttatctaa aatattttaa a

51

<210> 34  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (33 is other entry)

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<223> Accession number cg43988115

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atgcttagat gtggtgctgt ggtgcagtgc atttatctaa aatattttaa a

51

<210> 35  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (36 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 35

tcatgagaca tgcacagccc gcatcccatg ctccgggcgg ggatcgggag c 51

<210> 36  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (35 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27783345

<400> 36  
tcatgagaca tgcacagccc gcatcacatg ctccgggcgg ggatcgggag c 51

<210> 37  
<211> 51  
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<220>  
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<221> misc\_feature  
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<400> 37  
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<210> 38  
<211> 50  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg27783345

<400> 38  
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<210> 39  
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<223> Accession number cg43256113  
  
<400> 39  
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<210> 40  
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<222> (0)...(0)  
<223> Accession number cg43256113  
  
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<210> 41  
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<223> 1 of 2 allelic variants (42 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43256113  
  
<400> 41  
cttctgagtg agctgggact acaggtatat accactgcac ccagctgtaa g 51  
  
<210> 42  
<211> 51  
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<221> misc\_feature  
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<223> 2 of 2 allelic variants (41 is other entry)

<221> misc\_feature  
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<400> 42  
cttcctgagt agctgggact acaggcatat accactgcac ccagctgtaa g 51

<210> 43  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (44 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44023415

<400> 43  
ggaccggaga tggcgccgcc agcgggcgcg gcggcggcgg cggcctcgga c 51

<210> 44  
<211> 51  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44023415

<400> 44  
ggaccggaga tggcgccgcc agcggggcgg gcggcggcgg cggcctcgga c 51

<210> 45  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (46 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg44023415

<400> 45

accggagatg gcgccgccag cggcgcgggc gccggcggcg gcctcggact t

51

<210> 46

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (45 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44023415

<400> 46

accggagatg gcgccgccag cggcgggggc gccggcggcg gcctcggact t

51

<210> 47

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (48 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44929662

<400> 47

agcactttgg gaggccgagg caggcggatc accggaggtc aggagatcga g

51

<210> 48

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (47 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44929662

<400> 48

agcactttgg gaggccgagg caggcagatc accggaggtc aggagatcga g

51

<210> 49



<211> 51  
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<400> 49  
gcggatcacc ggaggtcagg agatcgagac catcctggcc aacatggtga a 51

<210> 50  
<211> 51  
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<220>  
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<400> 50  
gcggatcacc ggaggtcagg agatcaagac catcctggcc aacatggtga a 51

<210> 51  
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<220>  
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<223> 1 of 2 allelic variants (52 is other entry)

<221> misc\_feature  
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<223> Accession number cg29691725

<400> 51  
gggcatgggc cggccctctg tggcgccccg gaacttttcg caatcgcccc c 51

<210> 52  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (51 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 52  
gggcatgggc cggcctctg tggcggccg gaacttttcg caatcgccc c 51

<210> 53  
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<220>  
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<223> 1 of 2 allelic variants (54 is other entry)

<221> misc\_feature  
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<223> Accession number cg29691725

<400> 53  
aggcgccat caccgcgcg aaaacgttca tccccctcat cgacgggct c 51

<210> 54  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (53 is other entry)

<221> misc\_feature  
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<400> 54  
aggcgccat caccgcgcg aaaaccttca tccccctcat cgacgggct c 51

<210> 55  
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<223> 1 of 2 allelic variants (56 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43985676

<400> 55  
aataaaaagta tcatgaaaaa acctatTTTT tttccactg tccttccact a 51

<210> 56  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (55 is other entry)

<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43985676

<400> 56  
aataaaaagta tcatgaaaaa acctatTTTT tttccactgt ccttccacta 50

<210> 57  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (58 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44010970

<400> 57  
tcctggtccc gaagatgggg ggggggggca gaggagatc ttcacagttt c 51

<210> 58  
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<212> DNA  
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<220>  
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<222> (26)...(0)  
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<221> misc\_feature  
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<221> misc\_feature.

<222> (0)...(0)  
<223> Accession number cg44010970

<400> 58  
tcctggtccc gaagatgggg gggggggcag agtgagatct tcacagtttc 50

<210> 59  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (60 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44010970

<400> 59  
cctggtcccc aagatggggg gggggggcag agtgagatct tcacagtttc c 51

<210> 60  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44010970

<400> 60  
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<210> 61  
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<220>  
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<223> 1 of 2 allelic variants (62 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44010970

<400> 61  
ctggtcccga agatgggggg ggggggcaga gtgagatctt cacagtttcc a 51

<210> 62  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (61 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44010970

<400> 62  
ctggtcccga agatgggggg gggggcagag tgagatcttc acagtttcca 50

<210> 63  
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<223> 1 of 2 allelic variants (64 is other entry)

<221> misc\_feature  
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<223> Accession number cg42718385

<400> 63  
tattttgtag agatgggggt ttgccgtgtt atccaggctg gttttgaact c 51

<210> 64  
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<220>  
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<223> 2 of 2 allelic variants (63 is other entry)

<221> misc\_feature  
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<400> 64

tattttgtag agatgggggtt ttgccttggt atccaggctg gttttgaact c

51

<210> 65

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (66 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43263821

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51

<210> 66

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (65 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43263821

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aaacagcact cctcttctaa aaagacacac aggccgcctt tctcggcagt g

51

<210> 67

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (68 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg41644093

<400> 67

aagaccagcc tgggcaacat ggggaaaccc catctctaca aaaatacaaa a

51

<210> 68

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (67 is other entry)

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<223> Accession number cg41644093

<400> 68  
aagaccagcc tgggcaacat ggggagaccc catctctaca aaaatacaaa a 51

<210> 69  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg43284479

<400> 69  
cagtcgcatt taaaaaaatc aacaacaatg atgataatga aaaaatctga a 51

<210> 70  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (69 is other entry)

<221> misc\_feature  
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<223> Accession number cg43284479

<400> 70  
cagtcgcatt taaaaaaatc aacaagaatg atgataatga aaaaatctga a 51

<210> 71  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (72 is other entry)

<221> misc\_feature  
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<223> Accession number cg43284479

<400> 71  
ggaatgaaga gagaaagcag ctccccaact tcaaaacat tttggtacct g 51

<210> 72  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (71 is other entry)

<221> misc\_feature  
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<223> Accession number cg43284479

<400> 72  
ggaatgaaga gagaaagcag ctccctaact tcaaaacat tttggtacct g 51

<210> 73  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (74 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43971784

<400> 73  
gcacagctag gtaaaggggg aaaaaatcag atctcaagac agactctttg a 51

<210> 74  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (73 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg43971784

<400> 74

gcacagctag gtaaagggg aaaaatcaga tctcaagaca gactctttga

50

<210> 75

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (76 is other entry)

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<223> Accession number cg43971784

<400> 75

accggcacca aggcattgtct gccctaccca agaagggaga caggccctgg g

51

<210> 76

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (75 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43971784

<400> 76

accggcacca aggcattgtct gccctgccca agaagggaga caggccctgg g

51

<210> 77

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (78 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg42719787

<400> 77

tcaggctccc tagaattacc ccaaaggtca acactatctc agtgccagcc c

51

<210> 78

<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (77 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg42719787  
  
<400> 78  
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<210> 91  
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<210> 108  
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51

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50

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51

<210> 132

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (131 is other entry)

<221> misc\_feature  
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<223> Accession number cg42538578

<400> 132  
ttcaggaact ggggagaggc tggcttcttt ggaggctgag ctgacagagg c 51

<210> 133  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (134 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg42481111

<400> 133  
gcaagactcc acctcaaaaa aaaaaaccac aaaaaaacac aaaaggattc t 51

<210> 134  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg42481111

<400> 134  
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<210> 135  
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<212> DNA  
<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (136 is other entry)

<221> misc\_feature  
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<223> Accession number cg39710199

<400> 135  
caaaactcgac tcagcgggtga gctctagcac agttccatga gttgcgaccc t 51

<210> 136  
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<221> misc\_feature  
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<400> 136  
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<210> 137  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38821538

<400> 137  
aaaaaataat aataataata ataatttttt taaaaagagg tgtttttgag 50

<210> 138  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (137 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38821538

<400> 138

aaaaaataat aataataata ataatatattt ttaaaaagag gtgtttttga g

51

<210> 139

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38821538

<400> 139

aaaaaataat aataataata ataatttttt taaaaagagg tggtttttgag

50

<210> 140

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (139 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38821538

<400> 140

aaaaaataat aataataata ataatatattt ttaaaaagag gtgtttttga g

51

<210> 141

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (142 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38821538

<400> 141  
taataataat aataataatt tttttaaaaa gaggtgtttt tgaggtctta 50

<210> 142  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg38821538

<400> 142  
taataataat aataataatt tttttaaaaa agaggtgttt ttgaggtctt a 51

<210> 143  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (144 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg40038435

<400> 143  
tgatcctgca gaggagccaa aaaaaatctt aggtatagaa ctaatacaat t 51

<210> 144  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (143 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg40038435

<400> 144

tgatcctgca gaggagccaa aaaaatctta ggtatagaac taatacaatt

50

<210> 145

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (146 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43963046

<400> 145

ggccctgtgg ttagcatccc ccacacccat atcagccact agcatttttaa a

51

<210> 146

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (145 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43963046

<400> 146

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<210> 147

<211> 51

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<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (148 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43963046

<400> 147  
ccctgtgggtt agcatccccc acacccatat cagccactag catttttaaag a 51

<210> 148  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (147 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg43963046

<400> 148  
ccctgtgggtt agcatccccc acaccatata agccactagc attttaaaga 50

<210> 149  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (150 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43979733

<400> 149  
aaaatgtatg atcaagtccc agaaaacttt gccttcccaa ggaatgtgtt t 51

<210> 150  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (149 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43979733

<400> 150

aaaatgtatg atcaagtccc agaaactttg ccttcccaag gaatgtgtt

50

<210> 151

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

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<223> 1 of 2 allelic variants (152 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43979733

<400> 151

ccaaaaatca cattctctct ctctctctc tcctctctac cattctctc a

51

<210> 152

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (151 is other entry)

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<222> (25)...(26)

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43979733

<400> 152

ccaaaaatca cattctctct ctctccctct cctctctacc attctctca

50

<210> 153

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (154 is other entry)

<221> misc\_feature  
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<223> Accession number cg43979733

<400> 153  
cagtaagaaa accaggagac tccttctgaa aggcttccac ctgggaggaa a 51

<210> 154  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (153 is other entry)

<221> misc\_feature  
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<223> Accession number cg43979733

<400> 154  
cagtaagaaa accaggagac tccttatgaa aggcttccac ctgggaggaa a 51

<210> 155  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (156 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg42286566

<400> 155  
ctgggattac aggcatgagc caccgtgcct ggccagaaaa ttgtaaacac a 51

<210> 156  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (155 is other entry)

<221> misc\_feature  
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<223> Accession number cg42286566

<400> 156  
ctgggattac aggcatgagc caccgggcct ggccagaaaa ttgtaaacac a 51

<210> 157  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (158 is other entry)

<221> misc\_feature  
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<223> Accession number cg42286566

<400> 157  
gattacaggc atgagccacc gtgcctggcc agaaaattgt aaacacacac a 51

<210> 158  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (157 is other entry)

<221> misc\_feature  
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<223> Accession number cg42286566

<400> 158  
gattacaggc atgagccacc gtgcccggcc agaaaattgt aaacacacac a 51

<210> 159  
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<220>  
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<221> misc\_feature  
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<400> 159  
tgcctggcca gaaaattgta aacacacaca aactctcaag tggcctaatt c 51

<210> 160  
<211> 51  
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<221> misc\_feature  
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<400> 160  
tgcctggcca gaaaattgta aacacgcaca aactctcaag tggcctaatt c 51

<210> 161  
<211> 51  
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<220>  
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<221> misc\_feature  
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<400> 161  
ctctcaccaa accaatcaca atacagataa aagagaataa cttgtgttca t 51

<210> 162  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (161 is other entry)

<221> misc\_feature  
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<400> 162  
ctctcaccaa accaatcaca atacaaataa aagagaataa cttgtgttca t 51

<210> 163  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (164 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg42286566

<400> 163  
caatacagat aaaagagaat aacttgtgtt catttttgta caaacaaaaa a 51

<210> 164  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (163 is other entry)

<221> misc\_feature  
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<223> Accession number cg42286566

<400> 164  
caatacagat aaaagagaat aacttatgtt catttttgta caaacaaaaa a 51

<210> 165  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (166 is other entry)

<221> misc\_feature  
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<223> Accession number cg42286566

<400> 165  
atacagataa aagagaataa cttgtgttca tttttgtaca aacaaaaaag a 51

<210> 166  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (165 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg42286566

<400> 166  
atacagataa aagagaataa cttgtattca tttttgtaca aacaaaaaag a 51

<210> 167  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (168 is other entry)

<221> misc\_feature  
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<223> Accession number cg42286566

<400> 167  
cagataaaag agaataactt gtgttcattt ttgtacaaac aaaaaagata t 51

<210> 168  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 168  
cagataaaag agaataactt gtgttaattt ttgtacaaac aaaaaagata t 51

<210> 169  
<211> 50  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<221> misc\_feature  
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<400> 169  
ttcatttttg tacaacaaa aaagatataa attgtgaatg atgcatgatt 50

<210> 170  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (169 is other entry)

<221> misc\_feature  
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<400> 170  
ttcatttttg tacaacaaa aaagactata aattgtgaat gatgcatgat t 51

<210> 171  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (172 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg42468290

<400> 171  
caaaccaaac aaccacaaca aaaaaatccc tcacttttgt ttctgttta t 51

<210> 172  
<211> 50  
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<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (171 is other entry).

<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg42468290

<400> 172  
caaaccaaac aaccacaaca aaaaatccct cacttttggt ttctgtttat 50

<210> 173  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (174 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44010179

<400> 173  
tcccataggt agcagtcct gtgggcaggt ggaagggtgcc cgtccctcta g 51

<210> 174  
<211> 50  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (173 is other entry)

<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44010179

<400> 174  
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<210> 175  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (176 is other entry)

<221> misc\_feature  
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<400> 175  
cctaggagga agacaagctt gaaggacgac ccttaataaa gagcttctag g 51

<210> 176  
<211> 51  
<212> DNA  
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<220>



<221> misc\_feature  
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<223> 2 of 2 allelic variants (175 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg42927851

<400> 176  
cctaggagga agacaagctt gaagggcgac ccttaataaa gagcttctag g 51

<210> 177  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (178 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43998776

<400> 177  
tgatggggag ttttagagga gcaataaaaa acttccttct ttgtgcttgt g 51

<210> 178  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (177 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43998776

<400> 178  
tgatggggag ttttagagga gcaatcaaaa acttccttct ttgtgcttgt g 51

<210> 179  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (180 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg43923142

<400> 179  
cccactcgcg ttctgagccc cgagagcgtc ccgcacgctc agtttggtg a 51

<210> 180  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (179 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 180  
cccactcgcg ttctgagccc cgagaccgtc ccgcacgctc agtttggtg a 51

<210> 181  
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<220>  
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<223> 1 of 2 allelic variants (182 is other entry)

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<223> Accession number cg10053419

<400> 181  
gggggaggta ggcagtaccc cccctgctc ctgtggggaa ataggggctt a 51

<210> 182  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<400> 182  
gggggaggta ggcagtagcc ccccgctcc tgggggaaa taggggctta 50

<210> 183  
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<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (184 is other entry)

<221> misc\_feature  
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<223> Accession number cg10333107

<400> 183  
tgccctgag gtcaagcaga cccacaccgt cgaccgggtt gtcgtcgtaa c 51

<210> 184  
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<220>  
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<223> 2 of 2 allelic variants (183 is other entry)

<221> misc\_feature  
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<223> Accession number cg10333107

<400> 184  
tgccctgag gtcaagcaga cccacccgt cgaccgggtt gtcgtcgtaa c 51

<210> 185  
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<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (186 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg10353763

<400> 185  
tggcaggctt tgtcagtgtt tcagcgggta agaaatcttg actagtagga a 51

<210> 186  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (185 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg10353763

<400> 186  
tggcaggctt tgtcagtgtt tcagcaggta agaaatcttg actagtagga a 51

<210> 187  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (188 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg10854402

<400> 187  
ttgtgatctc aacaacaaca ttgaaaacag caggagcacc aggaccgatc t 51

<210> 188  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (187 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg10854402

<400> 188  
ttgtgatctc aacaacaaca ttgaatacag caggagcacc aggaccgatc t 51

<210> 189  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (190 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg11763542

<400> 189  
aggctgaggc aggagaatcg cttgagcctg ggaggcagag gttgcagtga g 51

<210> 190  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (189 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 190  
aggctgaggc aggagaatcg cttgaacctg ggaggcagag gttgcagtga g 51

<210> 191  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (192 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg11763542

<400> 191  
cgcttgagcc tgggaggcag aggttgagc gagccaagat catgccactg c 51

<210> 192  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (191 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg11763542

<400> 192

cgcttgagcc tgggaggcag aggttttcagt gagccaagat catgccactg c 51

<210> 193  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (194 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg11794373

<400> 193  
ccggaatacc ttatactttt tccccctttt ttttggggga aggaatgtgt g 51

<210> 194  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (193 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg11794373

<400> 194  
ccggaatacc ttatactttt tccccctttt ttttggggga aggaatgtgt g 51

<210> 195  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (196 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg11801777

<400> 195  
accctatcaa cccattaaaa tggattttta tgaattgata ataggggctc a 51

<210> 196  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (195 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg11801777

<400> 196  
accctatcaa cccattaaaa tggatattaa tgaattgata ataggggctc a 51

<210> 197  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (198 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg11801777

<400> 197  
tcaatcagct gataaacccc ctaaaaaagt tgcggaaacc caattgttac a 51

<210> 198  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (197 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg11801777

<400> 198  
tcaatcagct gataaacccc ctaaagaagt tgcggaaacc caattgttac a 51

<210> 199  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (200 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg12991942

<400> 199  
agagttttat tcctttgagg gccacagaag aaagtagtct agctctcttc a 51

<210> 200  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (199 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg12991942

<400> 200  
agagttttat tcctttgagg gccactgaag aaagtagtct agctctcttc a 51

<210> 201  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (202 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg13084930

<400> 201  
ttgttggtgcg tgtggtcaag atgctgactc acgatcacag tgggctcttc g 51

<210> 202  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (201 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg13084930

<400> 202  
ttgttggtgcg tgtggtcaag atgctaactc acgatcacag tgggctcttc g 51



<210> 203  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (204 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg13086160

<400> 203  
actaagcaca ggctcagccc cggtcgccat gcgcccaggc tcggttatca g

51

<210> 204  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (203 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg13086160

<400> 204  
actaagcaca ggctcagccc cggtcacccat gcgcccaggc tcggttatca g

51

<210> 205  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (206 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg13502101

<400> 205  
gcgggggttaa cgggtcagga gacaagaagg tgggtggtagt tgggtcgtag a

51

<210> 206  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (205 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg13502101

<400> 206  
gcgggggtaa cgggtcagga gacaaaaagg tgggtgtagt tgggtcgtag a 51

<210> 207  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (208 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14203037

<400> 207  
agtaacagaa atataacaaa attggcataa acatttgggt atctgttaac c 51

<210> 208  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (207 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14203037

<400> 208  
agtaacagaa atataacaaa attggaataa acatttgggt atctgttaac c 51

<210> 209  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (210 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg14203037

<400> 209  
agaaatataa caaaattggc ataaacattt gggatatctgt taaccaagag t 51

<210> 210  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (209 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14203037

<400> 210  
agaaatataa caaaattggc ataaaaattt gggatatctgt taaccaagag t 51

<210> 211  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (212 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14203037

<400> 211  
cataaacatt tgggtatctg ttaaccaaga gtgtgaagat aaggtagttc c 51

<210> 212  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (211 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14203037

<400> 212  
cataaacatt tgggtatctg ttaacaaaga gtgtgaagat aaggtagttc c 51

<210> 213  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (214 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14369904  
  
<400> 213  
gcggaacctc gcgcttcgcc cgggggacaa tccgaagtcg gcgctatgga a 51  
  
<210> 214  
<211> 50  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (213 is other entry)  
  
<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14369904  
  
<400> 214  
gcggaacctc gcgcttcgcc cgggggacaat ccgaagtcg cgctatggaa 50  
  
<210> 215  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (216 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14395282  
  
<400> 215  
caccctgat gccggcctgg ctgggaatgg gcccgctctg cacctcgagc t 51  
  
<210> 216  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (215 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14395282

<400> 216  
cacccctgat gccggcctgg ctgggggatgg gcccgctctg cacctcgagc t 51

<210> 217  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (218 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14395282

<400> 217  
cacctcgagc tagggcaaga agaggcagag ctggaggagt tcctgtgccc 50

<210> 218  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (217 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 218  
cacctcgagc tagggcaaga agaggacaga gctggaggag ttctgtgcc c 51

<210> 219  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (220 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14396111

<400> 219  
tcagatatgg aactacatga gatctgtagc gaactgcgga ggatcagaca c 51

<210> 220  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (219 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg14396111

<400> 220  
tcagatatgg aactacatga gatcttagcg aactgcggag gatcagacac 50

<210> 221  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg16311688

<400> 221  
gttctcgggt gccgtcgtg tgcgcttcgc tgctgtgacg ctcaactgggc g 51

<210> 222  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (221 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 222  
gttctcgggt gccgtcgtg tgcgcctcgc tgctgtgacg ctactgggc g 51

<210> 223  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (224 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16311688

<400> 223  
ggtccagtc ccacagttcg accacatccg gcggctccgt gcccgcgacc a 51

<210> 224  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (223 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16311688

<400> 224  
ggtccagtc ccacagttcg accacttccg gcggctccgt gcccgcgacc a 51

<210> 225  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (226 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg16311688

<400> 225

tgtccattgc gggtagtatt cggggcgcg gaagccgggg gttccactag g

51

<210> 226

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (225 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg16311688

<400> 226

tgtccattgc gggtagtatt cggggcgcg gaagccgggg gttccactag g

51

<210> 227

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (228 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg16311688

<400> 227

gggcgcgcga agccgggggt tccactaggg ctgggagccc gacaccgagc g

51

<210> 228

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (227 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg16311688

<400> 228

gggcgcgcga agccgggggt tccacgaggg ctgggagccc gacaccgagc g

51

<210> 229



<211> 51  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (230 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16392609

<400> 229  
tgctcattga tccctacgac aagggtgtca tggctcatga caggggtgggc g

51

<210> 230  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (229 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16392609

<400> 230  
tgctcattga tccctacgac aagggtgtca tggctcatga caggggtgggc g

51

<210> 231  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (232 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16392609

<400> 231  
cctacgacaa ggttggtcatg gctcatgaca ggggtggtcgc ggttcccact g

51

<210> 232  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 2 of 2 allelic variants (231 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16392609

<400> 232  
cctacgacaa ggttgatcatg gctcaagaca ggggtggcgc ggttcccact g 51

<210> 233  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (234 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16392609

<400> 233  
acaaggttgt catggctcat gacaggggtg tgcgggttcc cactgagggt g 51

<210> 234  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (233 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16392609

<400> 234  
acaaggttgt catggctcat gacagagtgg tgcgggttcc cactgagggt g 51

<210> 235  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (236 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16697187

<400> 235  
atgtgttcat tgccatcggg tcgatcctgc tcatcactgg attcggtgac g 51

<210> 236  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (235 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16697187

<400> 236  
atgtgttcat tgccatcggg tcgattctgc tcatcactgg attcggtgac g 51

<210> 237  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (238 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16843354

<400> 237  
aaaagactag taacggcgaa gccgacgaga cagttatctg ccacgttgct g 51

<210> 238  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (237 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16843354

<400> 238  
aaaagactag taacggcgaa gccgatgaga cagttatctg ccacgttgct g 51

<210> 239  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (240 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16845019

<400> 239  
cctctctgat atttgggtgg ggaagggggg ttgggggtcc tctttcttca a

51

<210> 240  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (239 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg16845019

<400> 240  
cctctctgat atttgggtgg ggaagtgggg ttgggggtcc tctttcttca a

51

<210> 241  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (242 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg17201640

<400> 241  
ccagttcata ttgatccaat ttctagaaaa caaatgctga agttcattgc a

51

<210> 242  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)

<223> 2 of 2 allelic variants (241 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg17201640

<400> 242

ccagttcata ttgatccaat ttctaaaaaa caaatgctga agttcattgc a

51

<210> 243

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (244 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg17872027

<400> 243

tgacttcaag tgatcctcct gcctcggcct ctcaaagtgc tgggattaca g

51

<210> 244

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (243 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg17872027

<400> 244

tgacttcaag tgatcctcct gcctcagcct ctcaaagtgc tgggattaca g

51

<210> 245

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (246 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg17872027

<400> 245  
caagtgatcc tcttgctcgc gcctctcaaa gtgctgggat tacagatatg a 51

<210> 246  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (245 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg17872027

<400> 246  
caagtgatcc tcttgctcgc gcctcccaaa gtgctgggat tacagatatg a 51

<210> 247  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (248 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg17964567

<400> 247  
gcctgtcca cactcagctc ccacagcctc accctgtccc accagacaca c 51

<210> 248  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (247 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg17964567

<400> 248  
gcctgtcca cactcagctc ccacatcctc accctgtccc accagacaca c 51

<210> 249  
<211> 46  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (250 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg17964567

<400> 249

gtcccaccag acacacacag cttagtgcaca cagattctgg aagctt

46

<210> 250

<211> 46

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (249 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg17964567

<400> 250

gtcccaccag acacacacag cttagcgaca cagattctgg aagctt

46

<210> 251

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (252 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg17964567

<400> 251

gctgaggcct gagcccatca aagacgagaa ctgactgagc acacctgggc a

51

<210> 252

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (251 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg17964567

<400> 252  
gctgaggcct gagcccatca aagacaagaa ctgactgagc acacctgggc a 51

<210> 253  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (254 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19426737

<400> 253  
cgttcagctc tgccaatggg aagccggagg cgcttccttc agcgagaagg t 51

<210> 254  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (253 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19426737

<400> 254  
cgttcagctc tgccaatggg aagccagagg cgcttccttc agcgagaagg t 51

<210> 255  
<211> 40  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (15)...(0)  
<223> 1 of 2 allelic variants (256 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19540358

<400> 255



nggagagacg acaaggggtga agggaaagaa tgactgatgg

40

<210> 256

<211> 40

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (15)...(0)

<223> 2 of 2 allelic variants (255 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg19540358

<400> 256

nggagagacg acaacggtga agggaaagaa tgactgatgg

40

<210> 257

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (258 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg19636928

<400> 257

ctatcagagg gctccatcac tccatcgtaa ggaggcagct ggtggcgagt c

51

<210> 258

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (257 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg19636928

<400> 258

ctatcagagg gctccatcac tccattgtaa ggaggcagct ggtggcgagt c

51

<210> 259

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (260 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19650073

<400> 259  
agctttggca gaggaccctc tgcacgcttc ctctcctcta gccagagctt c 51

<210> 260  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (259 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19650073

<400> 260  
agctttggca gaggaccctc tgcacacttc ctctcctcta gccagagctt c 51

<210> 261  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (262 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 261  
acgccgaccg gatcgtcgat cccattactc gggatctgct ggaatccctg g 51

<210> 262  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (261 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 262  
acgccgaccg gatcgtcgat cccatcactc gggatctgct ggaatccctg g 51

<210> 263  
<211> 39  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (14)...(0)  
<223> 1 of 2 allelic variants (264 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 263  
acgcgtccgc tccggatttc gttgacgagc tgcgctcag 39

<210> 264  
<211> 39  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (14)...(0)  
<223> 2 of 2 allelic variants (263 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 264  
acgcgtccgc tcccgatttc gttgacgagc tgcgctcag 39

<210> 265  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (266 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 265  
ctcgggatct gctggaatcc ctggttcgcg aagccggcga ggctgcggtg a 51

<210> 266  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (265 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 266  
ctcgggatct gctggaatcc ctggtccgcg aagccggcga ggctgcggtg a 51

<210> 267  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (268 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 267  
ctgctggaat ccctggttcg cgaagccggc gaggctgcgg tgatcttggg t 51

<210> 268  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (267 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 268  
ctgctggaat ccctggttcg cgaagtcggc gaggctgcgg tgatcttggg t 51

<210> 269  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (270 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 269  
tcacccatct gccccgacga cccagtaaac gtccccggct gttcctcatt g 51

<210> 270  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (269 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19847826

<400> 270  
tcacccatct gccccgacga cccagcaaac gtccccggct gttcctcatt g 51

<210> 271  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (272 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 271  
accgcgacgc gattctggcc ttccccgttg agacggtgta taccgccgac c 51

<210> 272  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (271 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg19848544

<400> 272  
accgcgacgc gattctggcc ttccctgttg agacggtgta taccgccgac c 51

<210> 273  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (274 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 273  
tctggccttc cccgttgaga cgggtgtatac cgccgaccgc cccgtgcagc g 51

<210> 274  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (273 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 274  
tctggccttc cccgttgaga cgggtgcatac cgccgaccgc cccgtgcagc g 51

<210> 275  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (276 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 275  
taccgccgac cgccccgtgc agcgccctggc cgaaatcggt gccgagtacg a 51

<210> 276  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (275 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 276  
taccgccgac cgccccgtgc agcgcttggc cgaaatcggt gccgagtacg a

51

<210> 277  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (278 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 277  
acgaaccggt tgaagtcac atgggacttc cggtcgccct taacgggact g

51

<210> 278  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (277 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 278  
acgaaccggt tgaagtcac atggggcttc cggtcgccct taacgggact g

51

<210> 279  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>

<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (280 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 279  
ttgaagtcacat catgggactt ccggtcgccc ttaacgggac tgagcagttg g

51

<210> 280  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (279 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 280  
ttgaagtcacat catgggactt ccggttgccc ttaacgggac tgagcagttg g

51

<210> 281  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (282 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19848544

<400> 281  
cggacacgtg tctgtgcggt gtgaggcttg ccatcgactg gggaaaggca c

51

<210> 282  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (281 is other entry)

<221> misc\_feature  
<222> (0)...(0)



<223> Accession number cg19848544

<400> 282

cggaacagtg tctgtgcggt gtgagacttg ccatcgactg gggaaaggca c

51

<210> 283

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (284 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg19869623

<400> 283

cagagtctgt gagcgccag gaggcacct gctcgactgg cccgtcctct c

51

<210> 284

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (283 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg19869623

<400> 284

cagagtctgt gagcgccag gaggcacctg ctgcactggc ccgtcctctc

50

<210> 285

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (286 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg19891431

<400> 285  
cttcaggagg ccaaggaggg aggatagact aaggtgagtt caagaccagc c 51

<210> 286  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (285 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19891431

<400> 286  
cttcaggagg ccaaggaggg aggatggact aaggtgagtt caagaccagc c 51

<210> 287  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (288 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19891431

<400> 287  
caagaccagc ctgggcaata cagtggagacc ctgcctctat aaaaaaaaaat t 51

<210> 288  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (287 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19891431

<400> 288  
caagaccagc ctgggcaata cagtgggacc ctgcctctat aaaaaaaaaat t 51

<210> 289  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (290 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg19906230

<400> 289

cagactgaca agcaagggat tttttccact caccgtcagt gggatgggtc t

51

<210> 290

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (289 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg19906230

<400> 290

cagactgaca agcaagggat ttttttcact caccgtcagt gggatgggtc t

51

<210> 291

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (292 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg19906230

<400> 291

acacgattat ttcacaaaaa gaaactttct gtgggacgtg cctgggcgac t

51

<210> 292

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (291 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19906230

<400> 292  
acacgattat ttcacaaaaa gaaaccttct gtgggacgtg cctgggcgac t 51

<210> 293  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (294 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19906230

<400> 293  
gccagcaaaa ctgagaacct tgttcgcaaa tccgtaccct ctcccaaggc a 51

<210> 294  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (293 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19906230

<400> 294  
gccagcaaaa ctgagaacct tgttctcaaa tccgtaccct ctcccaaggc a 51

<210> 295  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (296 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg19906230

<400> 295

aaactgagaa ccttgttcgc aaatccgtac cctctcccaa ggcagcctca g

51

<210> 296

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

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<223> Accession number cg19906230

<400> 296

aaactgagaa ccttgttcgc aaatctgtac cctctcccaa ggcagcctca g

51

<210> 297

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (298 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg20177119

<400> 297

ctcagaacct ggagatcagg ttttgaccgg tgagccagcc cgggaccttc c

51

<210> 298

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (297 is other entry)

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<223> Accession number cg20177119

<400> 298

ctcagaacct ggagatcagg ttttggccgg tgagccagcc cgggaccttc c

51

<210> 299

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature  
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<400> 299  
cagccgacgt cgcggctgac gacgtccccc ccaaaccgt tggcgatac c 51

<210> 300  
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<221> misc\_feature  
<222> (0)...(0)  
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<400> 300  
cagccgacgt cgcggctgac gacgtccccc caaatccgtt gggcgatacc 50

<210> 301  
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<221> misc\_feature  
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<400> 301  
acgtcgcggc tgacgacgtc ccccccaaat ccgttgggcg ataccgcct c 51

<210> 302  
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<221> misc\_feature  
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acgtcgcggc tgacgacgtc cccccaaatc cgttgggcga taccgcctc

50

<210> 303  
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<400> 303  
tcccccccaa atccgttggg cgataccgc ctogaaccaa cccgggattg a

51

<210> 304  
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<212> DNA  
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<400> 304  
tcccccccaa atccgttggg cgatatccgc ctogaaccaa cccgggattg a

51

<210> 305  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg20177119

<400> 305

ttgggcgata cccgcctcga accaaccg gattgacccc gggagatcca a

51

<210> 306

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (0)...(0)

<223> Accession number cg20177119

<400> 306

ttgggcgata cccgcctcga accaatccg gattgacccc gggagatcca a

51

<210> 307

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (308 is other entry)

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<223> Accession number cg20283978

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aggaaacacc agatttgccc aggaagacag tgggatggct ttgatatctc t

51

<210> 308

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<212> DNA

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<223> 2 of 2 allelic variants (307 is other entry)

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<222> (0)...(0)

<223> Accession number cg20283978



<400> 308  
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<210> 309  
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<221> misc\_feature  
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<223> Accession number cg20287156

<400> 309  
cggcggccca atctgccgga cgtgacgccg ggatgtcgct gggacttatg t 51

<210> 310  
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<221> misc\_feature  
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<223> Accession number cg20287156

<400> 310  
cggcggccca atctgccgga cgtgatgccg ggatgtcgct gggacttatg t 51

<210> 311  
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<212> DNA  
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<221> misc\_feature  
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<223> Accession number cg20287300

<400> 311  
ttgcggcccg atttcgactt tatcagtctc ttccacggag tcgacgagag a 51

<210> 312  
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<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (311 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg20287300

<400> 312

ttgccggccg atttcgactt tatcaatctc ttccacggag tcgacgagag a

51

<210> 313

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (314 is other entry)

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<222> (0)...(0)

<223> Accession number cg20289946

<400> 313

tccaggctgt gagcgtgcaa gaacagcacg gcggcgaaag agaaccggt a

51

<210> 314

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (313 is other entry)

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<223> Accession number cg20289946

<400> 314

tccaggctgt gagcgtgcaa gaacaccacg gcggcgaaag agaaccggt a

51

<210> 315

<211> 51

<212> DNA

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<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (316 is other entry)

<221> misc\_feature  
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<223> Accession number cg20289946

<400> 315  
gagcgtgcaa gaacagcacg gggcgaaaag agaaccgggt acgcggtgcg g 51

<210> 316  
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<220>  
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<400> 316  
gagcgtgcaa gaacagcacg gggccaaaag agaaccgggt acgcggtgcg g 51

<210> 317  
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<221> misc\_feature  
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<400> 317  
ggatctgtgg ccacctctc aagggttgcc acacgcacca ggtcctgact g 51

<210> 318  
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<221> misc\_feature  
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<400> 318

ggatctgtgg ccacctctc aaggggtgcc acacgcacca ggtcctgact g

51

<210> 319

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> Accession number cg20375502

<400> 319

cgaccaggt cctgactggg agtccggccc ccagggcctg tggatggctg g

51

<210> 320

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (319 is other entry)

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<223> Accession number cg20375502

<400> 320

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<210> 321

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (322 is other entry)

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<223> Accession number cg20436198

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51

<210> 322

<211> 50

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<223> Accession number cg20436198

<400> 322  
aagttttcct cgagaagcct ggcacatct ccgagagggc gcctggagcg 50

<210> 323  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 323  
gggcccggtg gggctctgcg gggacgcggg cgaggacggc gcggacgagg c 51

<210> 324  
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<221> misc\_feature  
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<400> 324  
gggcccggtg gggctctgcg gggaccgggc gaggacggcg cggacgaggc 50

<210> 325  
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<212> DNA  
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<223> 1 of 2 allelic variants (326 is other entry)

<221> misc\_feature  
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<223> Accession number cg20436638

<400> 325  
ctaccaggcc gccgccttcg ccggatcccg tcccgacctt gagttgggtc a

51

<210> 326  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (325 is other entry)

<221> misc\_feature  
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<400> 326  
ctaccaggcc gccgccttcg ccggaaccg tcccgacctt gagttgggtc a

51

<210> 327  
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<400> 327  
ccgccgcctt ccgccgatcc cgtcccgacc ttgagttggt tcagctgaat t

51

<210> 328  
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<223> Accession number cg20436638

<400> 328

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<210> 329

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (330 is other entry)

<221> misc\_feature

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<223> Accession number cg20440553

<400> 329

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51

<210> 330

<211> 51

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<223> Accession number cg20440553

<400> 330

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51

<210> 331

<211> 51

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<223> 1 of 2 allelic variants (332 is other entry)

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<222> (0)...(0)

<223> Accession number cg20442259

<400> 331  
cggccactcc ccatcgcccta tgaggcgacc atcatcacct tcaccgaaca a 51

<210> 332  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20442259

<400> 332  
cggccactcc ccatcgcccta tgagggacca tcatcacctt caccgaacaa 50

<210> 333  
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<221> misc\_feature  
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<400> 333  
ggggagagag gcgggaggga cactggcctg gagagaggcg ggagggacgc t 51

<210> 334  
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<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (333 is other entry)

<221> misc\_feature  
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<223> Accession number cg20452710

<400> 334  
ggggagagag gcgggaggga cactgacctg gagagaggcg ggagggacgc t 51



<210> 335  
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<223> Accession number cg20457127  
  
<400> 335  
cgaggaaatg acctccttcg cggtagccga ccagcgatcc accgacgaga c 51  
  
<210> 336  
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<210> 337  
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<223> 1 of 2 allelic variants (338 is other entry)  
  
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<223> Accession number cg20549295  
  
<400> 337  
ttagaggac aaggaagaag ccaggaagcc gccccaggcc cattgccatt g 51  
  
<210> 338

<211> 51  
<212> DNA  
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<223> 2 of 2 allelic variants (337 is other entry)

<221> misc\_feature  
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<400> 338  
ttagaggagac aaggaagaag ccaggagacc gccccaggcc cattgccatt g 51

<210> 339  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (340 is other entry)

<221> misc\_feature  
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<400> 339  
ttggtctttt gagatgggtt tcagactttt gcattatggc aaccaactga c 51

<210> 340  
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<400> 340  
ttggtctttt gagatgggtt tcagattttt gcattatggc aaccaactga c 51

<210> 341  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (342 is other entry)

<221> misc\_feature  
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<223> Accession number cg20562607

<400> 341  
tgagcttggt cacaccctct ggcaggaagt tcagaaggga acacagaacc a 51

<210> 342  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (341 is other entry)

<221> misc\_feature  
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<223> Accession number cg20562607

<400> 342  
tgagcttggt cacaccctct ggcagaaagt tcagaaggga acacagaacc a 51

<210> 343  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (344 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44921008

<400> 343  
aaaccaagt gtggcaaagg aactcattgc tctcgaaatg catatatggt g 51

<210> 344  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (343 is other entry)

<221> misc\_feature  
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<400> 344  
aaaccaagt gtggcaaagg aactcgttgc tctcgaaatg catatatgtt g 51

<210> 345  
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<220>  
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<223> 1 of 2 allelic variants (346 is other entry)

<221> misc\_feature  
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<223> Accession number cg44921017

<400> 345  
acatctgttt agccacagaa agcattgggc catactcact gcagaagata a 51

<210> 346  
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<220>  
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<223> Accession number cg44921017

<400> 346  
acatctgttt agccacagaa agcatcgggc catactcact gcagaagata a 51

<210> 347  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (348 is other entry)

<221> misc\_feature  
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<223> Accession number cg44921017

<400> 347  
gataagactt cctcagaatc ttattcggtt agtgcaactca attttacttc a 51

<210> 348  
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<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (347 is other entry)

<221> misc\_feature  
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<223> Accession number cg44921017

<400> 348  
gataagactt cctcagaatc ttatttggtt agtgactca attttacttc a 51

<210> 349  
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<212> DNA  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<400> 349  
ggatgcggac atcgacaagg ccttgcagga tctgctgggg caccttgaag c 51

<210> 350  
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<400> 350  
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<210> 351  
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<221> misc\_feature

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<223> Accession number cg44921180

<400> 351

tctgctgggg caccttgaag cggacatagg agcagagctg aagcatttca c

51

<210> 352

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (351 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44921180

<400> 352

tctgctgggg caccttgaag cggacgtagg agcagagctg aagcatttca c

51

<210> 353

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<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (354 is other entry)

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<223> Accession number cg44921180

<400> 353

tgaagcggac ataggagcag agctgaagca ttctactcat ctcttctggg g

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<223> 2 of 2 allelic variants (353 is other entry)

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<222> (0)...(0)

<223> Accession number cg44921180

<400> 354  
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<210> 355  
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<400> 355  
ggacatagga gcagagctga agcatttcac tcattctctc tggggtagac g 51

<210> 356  
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<221> misc\_feature  
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<400> 356  
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<210> 357  
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<400> 357  
gctgaagcat ttctactcatc tcttctgggg tagacgggat caagggaatc t 51

<210> 358  
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<210> 359

<211> 51

<212> DNA

<213> Homo sapiens

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<400> 359  
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<210> 360

<211> 51

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<223> Accession number cg44921180

<400> 360  
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<210> 361

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (362 is other entry)



<221> misc\_feature  
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<400> 361  
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<210> 362  
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<221> misc\_feature  
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<400> 362  
tctcttctg ggtagacggg atcaaaggaa tcttctccac ggcggcagag c 51

<210> 363  
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<221> misc\_feature  
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<223> Accession number cg44921180

<400> 363  
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<210> 364  
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<221> misc\_feature  
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<400> 364

tcctccctgg tcttgcagcc aatggactgc agtcatacat gggctcttat g

51

<210> 365

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44921801

<400> 365

gcctgggcaa caagagtga actccatctc aaaaaaaaaa aaaaaaaaag a

51

<210> 366

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (365 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44921801

<400> 366

gcctgggcaa caagagtga actccgtctc aaaaaaaaaa aaaaaaaaag a

51

<210> 367

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (368 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44921847

<400> 367

aataatatgt taacataaac ataacaacac acatattatt tttctacccc t

51

<210> 368

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature  
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<223> Accession number cg44921847

<400> 368  
aataatatgt taacataaac ataacgacac acatattatt tttctacccc t 51

<210> 369  
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<220>  
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<223> 1 of 2 allelic variants (370 is other entry)

<221> misc\_feature  
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<223> Accession number cg44921882

<400> 369  
aaaacttgaa ctcttctaga cagataccga gtggcaatct gggtatgttt g 51

<210> 370  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (369 is other entry)

<221> misc\_feature  
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<223> Accession number cg44921882

<400> 370  
aaaacttgaa ctcttctaga cagatcccga gtggcaatct gggtatgttt g 51

<210> 371  
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<221> misc\_feature  
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<223> Accession number cg44921882

<400> 371  
acagataccg agtggcaatc tgggtatggt tggcaatagc ggagcagcac a 51

<210> 372  
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<220>  
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<221> misc\_feature  
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<400> 372  
acagataccg agtggcaatc tgggtgtggt tggcaatagc ggagcagcac a 51

<210> 373  
<211> 51  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44921986

<400> 373  
cctgaatggg gtggtagatt ttttttctta aaaaaatttt tttgtttttt t 51

<210> 374  
<211> 50  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg44921986

<400> 374

cctgaatggg gtggtagatt tttttcttaa aaaaattttt ttgttttttt

50

<210> 375

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (376 is other entry)

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<223> Accession number cg44921986

<400> 375

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51

<210> 376

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (375 is other entry)

<221> misc\_feature

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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44921986

<400> 376

attttttttt ttaaaaaaat ttttttgttt ttttaatact cagaggagag

50

<210> 377

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (378 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44921986

<400> 377  
tttttttctt aaaaaaatTT ttttgTTTT ttttaactc agaggagagg g 51

<210> 378  
<211> 50  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44921986

<400> 378  
tttttttctt aaaaaaatTT ttttgTTTT ttaactca gaggagagg 50

<210> 379  
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<220>  
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<221> misc\_feature  
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<400> 379  
cttaaaaaaa tttttttgtt ttttttaata ctcagaggag agggacatag g 51

<210> 380  
<211> 50  
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<223> Accession number cg44921986

<400> 380  
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<210> 381  
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<400> 381  
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<210> 382  
<211> 51  
<212> DNA  
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<221> misc\_feature  
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<400> 382  
acgtggagac catcctgggc ctcacgggag cgaccatggg aagcctcatc t 51

<210> 383  
<211> 51  
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<221> misc\_feature  
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<400> 383  
cagcccaggc ccagtatgat accccgaaag ctgggaagcc aggtctacct g 51

<210> 384

<211> 51  
<212> DNA  
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<223> Accession number cg44922119  
  
<400> 384  
cagcccaggc ccagtatgat accccaaaag ctgggaagcc aggtctacct g 51  
  
<210> 385  
<211> 50  
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<223> Accession number cg44922119  
  
<400> 385  
aagcatcggt ttaaagcaca tggccttttt tttttaatta ttagtggtag 50  
  
<210> 386  
<211> 51  
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<223> Accession number cg44922119  
  
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<210> 387  
<211> 51  
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<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (388 is other entry)

<221> misc\_feature  
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<400> 387  
tttaaagcac atggcctttt ttttttaatt attagtggta gtaatatata g 51

<210> 388  
<211> 50  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature  
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<400> 388  
tttaaagcac atggcctttt tttttaatta ttagtggtag taatatatag 50

<210> 389  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<400> 389  
atgtggtgac tgaggtagac gaaactacta atcttgccat cttgctttaa g 51

<210> 390  
<211> 51  
<212> DNA  
<213> Homo sapiens

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<221> misc\_feature  
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<400> 390  
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<210> 391  
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<221> misc\_feature  
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<223> Accession number cg44922173

<400> 391  
tggctataaaa ttctcaatta tgatacgaac atttatttta caaattctac a 51

<210> 392  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (391 is other entry)

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<222> (0)...(0)  
<223> Accession number cg44922173

<400> 392  
tggctataaaa ttctcaatta tgatatgaac atttatttta caaattctac a 51

<210> 393  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (394 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg44923068

<400> 393  
ataaaaaccg gcacagcccg tctggcatgt ttgattatga ctttgagatt g 51

<210> 394  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (393 is other entry)

<221> misc\_feature  
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<400> 394  
ataaaaaccg gcacagcccg tctgggatgt ttgattatga ctttgagatt g 51

<210> 395  
<211> 51  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (396 is other entry)

<221> misc\_feature  
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<223> Accession number cg44923491

<400> 395  
gtaagcagag gtaccaaaga aagtactggg aggtgcagac tttgttaaaa g 51

<210> 396  
<211> 51  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg44923491

<400> 396  
gtaagcagag gtaccaaaga aagtattggg aggtgcagac tttgttaaaa g 51

<210> 397  
<211> 51  
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<223> 1 of 2 allelic variants (398 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44923661  
  
<400> 397  
atcacttagg accatcaaaa aaatgtgtac ctttctccaa acgacaactg a 51  
  
<210> 398  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
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<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (397 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44923661  
  
<400> 398  
atcacttagg accatcaaaa aaatgcgtac ctttctccaa acgacaactg a 51  
  
<210> 399  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (400 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44923666  
  
<400> 399  
attggtagca tgggttcact tggctacaac tgagcaaaat agatgcaact t 51  
  
<210> 400  
<211> 51  
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<213> Homo sapiens  
  
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<221> misc\_feature  
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<221> misc\_feature  
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attggttagca tgggttcact tggctgcaac tgagcaaat agatgcaact t 51

<210> 401  
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<220>  
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<223> 1 of 2 allelic variants (402 is other entry)

<221> misc\_feature  
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<223> Accession number cg44923675

<400> 401  
aagatttgaa gcaattggtg gagtcaacag aatgggaggt tagagaaaga t 51

<210> 402  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 402  
aagatttgaa gcaattggtg gagtcgacag aatgggaggt tagagaaaga t 51

<210> 403  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg44923675

<400> 403

gagattaagt acaaagtgag gaagatggaa gatgggtgaa tagtgctgaa t

51

<210> 404

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (403 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44923675

<400> 404

gagattaagt acaaagtgag gaagacggaa gatgggtgaa tagtgctgaa t

51

<210> 405

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (406 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44923758

<400> 405

acttaaataa cgccatgttt aatactgaca attatttgct aaccttaaga c

51

<210> 406

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (405 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44923758

<400> 406

acttaaataa cgccatgttt aatacagaca attatttgct aaccttaaga c

51

<210> 407

<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (408 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44923987

<400> 407  
ccactctttg gagaccatta tgatactatg accagagtac aggcaaaagg c 51

<210> 408  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (407 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44923987

<400> 408  
ccactctttg gagaccatta tgatattatg accagagtac aggcaaaagg c 51

<210> 409  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (410 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924189

<400> 409  
aggatgcact gagtcagagc taaggagggg tggacaagcg ctgaactctg c 51

<210> 410  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (409 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924189

<400> 410  
aggatgcact gagtcagagc taaggaaggg tggacaagcg ctgaactctg c 51

<210> 411  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (412 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924398

<400> 411  
ctgaggagcc aggagacagg ggaccggcca agggtcaccg gcaatcacat c 51

<210> 412  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (411 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924398

<400> 412  
ctgaggagcc aggagacagg ggaccgcca agggtcaccg gcaatcacat c 51

<210> 413  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (414 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924398



<400> 413  
agacagggga ccgccaagg gtcacggga atcacatcct taaagctgcc g 51

<210> 414  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (413 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924398

<400> 414  
agacagggga ccgccaagg gtcacggga atcacatcct taaagctgcc g 51

<210> 415  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (416 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924398

<400> 415  
gacaggggac attctctctc ctcacgggtg aggacagtta tcccaccagg t 51

<210> 416  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (415 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924398

<400> 416  
gacaggggac attctctctc ctcacagggtg aggacagtta tcccaccagg t 51

<210> 417  
<211> 51

<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (418 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924574

<400> 417  
aagacgaact gatccagccc cagctcggag agctctcagg agagaagctt c 51

<210> 418  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (417 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924574

<400> 418  
aagacgaact gatccagccc cagcttggag agctctcagg agagaagctt c 51

<210> 419  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (420 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924623

<400> 419  
gtgctgagat tacaggcatg aaccactgcc cttggacaag gcagggtttt a 51

<210> 420  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)

<223> 2 of 2 allelic variants (419 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44924623

<400> 420

gtgctgagat tacaggcatg aaccattgcc cttggacaag gcagggtttt a

51

<210> 421

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (422 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44924630

<400> 421

gcttttgggt gaagggtgat ttctactaga cacatctgtg cttcagtcac a

51

<210> 422

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (421 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44924630

<400> 422

gcttttgggt gaagggtgat ttctattaga cacatctgtg cttcagtcac a

51

<210> 423

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (424 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44924824

<400> 423  
ggggaggctg gagagtctgg gtggataccc tctcaatagc ccattccaag g 51

<210> 424  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (423 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924824

<400> 424  
ggggaggctg gagagtctgg gtggacaccc tctcaatagc ccattccaag g 51

<210> 425  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (426 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924824

<400> 425  
ccctctcaat agccattcc aaggctactt atgaagctca taaggaatac c 51

<210> 426  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (425 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924824

<400> 426  
ccctctcaat agccattcc aagggtactt atgaagctca taaggaatac c 51

<210> 427  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (428 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924824

<400> 427  
cccattccaa ggtcacttat gaagtcata aggaatacct agccaaaatg t 51

<210> 428  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (427 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924824

<400> 428  
cccattccaa ggtcacttat gaagcacata aggaatacct agccaaaatg t 51

<210> 429  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (430 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924824

<400> 429  
cttatgaagc tcataaggaa tacctagcca aaatgtatga ggaatatcaa a 51

<210> 430  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (429 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924824

<400> 430  
cttatgaagc tcataaggaa tacctggcca aaatgtatga ggaatatcaa a 51

<210> 431  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (432 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924824

<400> 431  
ggaatgtgag caccatctct ggtctttcat cacagacaac aggagcaaaa g 51

<210> 432  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (431 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924824

<400> 432  
ggaatgtgag caccatctct ggtctctcat cacagacaac aggagcaaaa g 51

<210> 433  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (434 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924961

<400> 433

aactcctggc ctcaagctat cctcccgct cagcctccca aagtgctgag a

51

<210> 434

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (433 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44924961

<400> 434

aactcctggc ctcaagctat cctcctgcct cagcctccca aagtgctgag a

51

<210> 435

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (436 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44925079

<400> 435

cttgggctcc cccttcattg cctctgcacc tccacactcc caaccactga c

51

<210> 436

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (435 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44925079

<400> 436

cttgggctcc cccttcattg cctctacacc tccacactcc caaccactga c

51

<210> 437

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (438 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925235

<400> 437  
tcgtgttaaa ctgatgtggc agtaaacc aa gggactaagc acatgattat t 51

<210> 438  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (437 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925235

<400> 438  
tcgtgttaaa ctgatgtggc agtaatccaa gggactaagc acatgattat t 51

<210> 439  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (440 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925358

<400> 439  
cggaactcgc tatatgcacg tgtgtgtgtc cgtatgtaag aaagtgtgca c 51

<210> 440  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (439 is other entry)



<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925358

<400> 440  
cggaactgc tatatgcacg tgtgtatgtc cgtatgtaag aaagtgtgca c 51

<210> 441  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (442 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925402

<400> 441  
acagaagatg ctaggtttgc acgctgatga gatcctggct aacactgctg c 51

<210> 442  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (441 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925402

<400> 442  
acagaagatg ctaggtttgc acgctaata ga gatcctggct aacactgctg c 51

<210> 443  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (444 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925402

<400> 443  
ttcaagactt cgagtttagac agaaaccag ggggctgcgg ctctggtggt t 51

<210> 444  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (443 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925402

<400> 444  
ttcaagactt cgagtttagac agaaatccag ggggctgcgg ctctggtggt t 51

<210> 445  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (446 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925406

<400> 445  
aaagagccaa ggcgctggac cagtccgaca acgatatgtc cgccgtgtac c 51

<210> 446  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (445 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925406

<400> 446  
aaagagccaa ggcgctggac cagtctgaca acgatatgtc cgccgtgtac c 51

<210> 447  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (448 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925534

<400> 447  
cttctataac ttacttgcca ctgccttttt tttttgatag aatcttgctc t 51

<210> 448  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (447 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925534

<400> 448  
cttctataac ttacttgcca ctgccttttt ttttgataga atcttgctct 50

<210> 449  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (450 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925534

<400> 449  
ttgccactgc cttttttttt tgatagaatc ttgctctgct gcccgagggtg g 51

<210> 450  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 2 of 2 allelic variants (449 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925534

<400> 450  
ttgccactgc cttttttttt tgataaaatc ttgctctgtc gccagggtg g 51

<210> 451  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (452 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925849

<400> 451  
gaatgccact tggatgacag ttctccctaa gacccccctt tcagcatggt t 51

<210> 452  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (451 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925849

<400> 452  
gaatgccact tggatgacag ttctctctaa gacccccctt tcagcatggt t 51

<210> 453  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (454 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925849

<400> 453  
gctggtgtcc tcctttggga tactctcacc ccttggttcc tcagatgaaa g 51

<210> 454  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (453 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44925849

<400> 454  
gctggtgtcc tcctttggga tactcccacc ccttggttcc tcagatgaaa g 51

<210> 455  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (456 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44926335

<400> 455  
cacacacaca cacacacaca cacaccctta cacgaatggt aatgaaatga 50

<210> 456  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (455 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44926335

<400> 456

cacacacaca cacacacaca cacacacctt acacgaatgg taatgaaatg a 51

<210> 457  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (458 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44927187

<400> 457  
ggctggggggg ctaagaagga gatcttgaga aggatggacc tgagctaaag a 51

<210> 458  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (457 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44927187

<400> 458  
ggctggggggg ctaagaagga gatctcgaga aggatggacc tgagctaaag a 51

<210> 459  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (460 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44927553

<400> 459  
actacaggca tgcaccacca caccagcta atttttgat ttttagtaga g 51

<210> 460  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (459 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44927553

<400> 460  
actacaggca tgcaccacca caccgggcta atttttgtat ttttagtaga g 51

<210> 461  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
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<221> misc\_feature  
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<223> Accession number cg44927553

<400> 461  
caccagcta atttttgtat ttttagtaga gacgggggtt catcatgttg g 51

<210> 462  
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<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (461 is other entry)

<221> misc\_feature  
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<223> Accession number cg44927553

<400> 462  
caccagcta atttttgtat ttttaataga gacgggggtt catcatgttg g 51

<210> 463  
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<212> DNA  
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<223> 1 of 2 allelic variants (464 is other entry)

<221> misc\_feature  
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<223> Accession number cg44927553

<400> 463  
accagctaa tttttgtatt tttagtagag acgggggtttc atcatgttg c 51

<210> 464  
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<212> DNA  
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<221> misc\_feature  
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<400> 464  
accagctaa tttttgtatt tttagagaga cgggggtttca tcatgttggc 50

<210> 465  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (466 is other entry)

<221> misc\_feature  
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<223> Accession number cg44927553

<400> 465  
acgggggtttc atcatgttg ccaggctggt ctcaaactcc tgacctcatg a 51

<210> 466  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (465 is other entry)

<221> misc\_feature  
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<223> Accession number cg44927553

<400> 466

acggggtttc atcatgttgg ccaggttggt ctcaaactcc tgacctcatg a

51

<210> 467

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (468 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928037

<400> 467

aaaaaagaaa agaaaagcaa aaaagaaaaa aaaaaggatt ggggtgggggg a

51

<210> 468

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (467 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928037

<400> 468

aaaaaagaaa agaaaagcaa aaaagaaaaa aaaaggattg ggtggggggga

50

<210> 469

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (470 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928037

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<210> 470  
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<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44928037

<400> 470  
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<210> 471  
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<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<400> 471  
tagatttcaa agatgaacct ggctctccat cactgagcca gacattcatt c 51

<210> 472  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<400> 472  
tagatttcaa agatgaacct ggctcccat cactgagcca gacattcatt c 51

<210> 473  
<211> 51  
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<223> 1 of 2 allelic variants (474 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44928115  
  
<400> 473  
catggtgact caagcctgta atcccagcac ttggggaggc cgaggcgggc g 51  
  
<210> 474  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
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<223> 2 of 2 allelic variants (473 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44928115  
  
<400> 474  
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<210> 475  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
<220>  
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<223> 1 of 2 allelic variants (476 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44928274  
  
<400> 475  
tgcagtgcac acgtggtatg catgtccggc attgatcaag tccatctggg c 51  
  
<210> 476  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (475 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44928274

<400> 476  
tgcagtgcac acgtggtatg catgttcggc attgatcaag tccatctggg c 51

<210> 477  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (478 is other entry)

<221> misc\_feature  
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<223> Accession number cg44928274

<400> 477  
gtccggcatt gatcaagtcc atctgggcta tggccataag ccaacaccag t 51

<210> 478  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (477 is other entry)

<221> misc\_feature  
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<400> 478  
gtccggcatt gatcaagtcc atctgagcta tggccataag ccaacaccag t 51

<210> 479  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928274

<400> 479

gcagagtaag tccaaaatcc atgcagcacg cagcctgagt gagatcgcca t

51

<210> 480

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (479 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928274

<400> 480

gcagagtaag tccaaaatcc atgcaacacg cagcctgagt gagatcgcca t

51

<210> 481

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (482 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928274

<400> 481

agacctcgaa gctggccaac atgggtagca aggggaagat catcagcggc a

51

<210> 482

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (481 is other entry)

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<222> (0)...(0)

<223> Accession number cg44928274

<400> 482

agacctcgaa gctggccaac atgggcagca aggggaagat catcagcggc a

51

<210> 483  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (484 is other entry)

<221> misc\_feature  
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<223> Accession number cg44928274

<400> 483  
aagatcatca gcggcagcag cggcagcctg ctgtcttcag gttctcagga a

51

<210> 484  
<211> 50  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
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<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44928274

<400> 484  
aagatcatca gcggcagcag cggcacctgc tgtcttcagg ttctcaggaa

50

<210> 485  
<211> 50  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg44928329

<400> 485

ttaagaagtg taaaaaaca caacgaaaa aaaccccaaa tcatggagaa

50

<210> 486

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (485 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928329

<400> 486

ttaagaagtg taaaaaaca caacgaaaa aaaaccccaa atcatggaga a

51

<210> 487

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (488 is other entry)

<221> misc\_feature

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<223> Accession number cg44928356

<400> 487

ccccaacgtg tacaagaaat ccaggaggaa aggccgtcaa ggtaaaaaat g

51

<210> 488

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (487 is other entry)

<221> misc\_feature

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<223> Accession number cg44928356

<400> 488

ccccaacgtg tacaagaaat ccagggggaa aggccgtcaa ggtaaaaaat g

51

<210> 489

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (490 is other entry)

<221> misc\_feature  
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<400> 489  
caacgtgtac aagaaatcca ggaggaaagg ccgtcaaggt aaaaaatgga a 51

<210> 490  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg44928356

<400> 490  
caacgtgtac aagaaatcca ggagggaagg ccgtcaaggt aaaaaatgga a 51

<210> 491  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (492 is other entry)

<221> misc\_feature  
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<400> 491  
gtcaaggtaa aaaatggaaa ttccctctgt tccaacgctg attgagtctg t 51

<210> 492  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (491 is other entry)



<221> misc\_feature  
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<223> Accession number cg44928356

<400> 492  
gtcaaggtaa aaaatggaaa ttcccgctgt tccaacgctg attgagtctg t 51

<210> 493  
<211> 51  
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<221> misc\_feature  
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<400> 493  
atggaaattc cctctgttcc aacgctgatt gagtctgttg tcttaaaaga g 51

<210> 494  
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<220>  
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<221> misc\_feature  
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<400> 494  
atggaaattc cctctgttcc aacgccgatt gagtctgttg tcttaaaaga g 51

<210> 495  
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<220>  
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<223> 1 of 2 allelic variants (496 is other entry)

<221> misc\_feature  
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<400> 495  
gaaattccct ctgttccaac gctgattgag tctgttgtct taaaagagct t 51

<210> 496  
<211> 51  
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<223> Accession number cg44928356  
  
<400> 496  
gaaattccct ctgttccaac gctgactgag tctgttgtct taaaagagct t 51  
  
<210> 497  
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<220>  
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<221> misc\_feature  
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<400> 497  
gttccaacgc tgattgagtc tgttgtctta aaagagcttt aaagggcccc c 51  
  
<210> 498  
<211> 51  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44928356  
  
<400> 498  
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<210> 499  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (500 is other entry)

<221> misc\_feature  
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<223> Accession number cg44928356

<400> 499  
ctgattgagt ctgttgcttt aaaagagctt taaagggcc cccttctttt c 51

<210> 500  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (499 is other entry)

<221> misc\_feature  
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<400> 500  
ctgattgagt ctgttgcttt aaaagggtt taaagggcc cccttctttt c 51

<210> 501  
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<220>  
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<223> 1 of 2 allelic variants (502 is other entry)

<221> misc\_feature  
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<400> 501  
agggccccc ttcttttcca gcactaccac tgccattcc agtcttgggt g 51

<210> 502  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928356

<400> 502

agggccccc ttcttttcca gcactccac tgccattcc agtcttgggt g

51

<210> 503

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

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<223> 1 of 2 allelic variants (504 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928665

<400> 503

caaagccaaa cttgcaccaa aaaaagggtc atggtcactg ttcggtgggtc t

51

<210> 504

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<221> misc\_feature

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928665

<400> 504

caaagccaaa cttgcaccaa aaaaagggtca tggtcactgt tcggtgggtct

50

<210> 505

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (506 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44928771

<400> 505  
agctggccag gcacttaatt tggggaaaga gaaggatttt gaggtaaact a 51

<210> 506  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (505 is other entry)

<221> misc\_feature  
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<223> Accession number cg44928771

<400> 506  
agctggccag gcacttaatt tgggggaaga gaaggatttt gaggtaaact a 51

<210> 507  
<211> 51  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
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<221> misc\_feature  
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<223> Accession number cg44929331

<400> 507  
gatgacagca actataaagg agagaagttt tcgttgaagt aactggaaa t 51

<210> 508  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (507 is other entry)

<221> misc\_feature  
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<223> Accession number cg44929331

<400> 508  
gatgacagca actataaagg agagaggttt tcgttgaagt aactggaaa t 51

<210> 509  
<211> 51

<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg44930314

<400> 509  
tgggcgtgtc ggtggtgacg caccctgggg gctgccgggg ccatgaggtg g 51

<210> 510  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (509 is other entry)

<221> misc\_feature  
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<400> 510  
tgggcgtgtc ggtggtgacg caccctgggg gctgccgggg ccatgaggtg g 51

<210> 511  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (512 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44930892

<400> 511  
gtgtacatat tccttgcat ttttttagtt gttgtcttaa aaaaaaaaaa a 51

<210> 512  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (511 is other entry)

<221> misc\_feature

<222> (25)...(26)

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44930892

<400> 512

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50

<210> 513

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (514 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44931317

<400> 513

aaaagttag tagagacatg gaagacgtaa aggggacccc aagcaagcct c

51

<210> 514

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (513 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44931317

<400> 514

aaaagttag tagagacatg gaagatgtaa aggggacccc aagcaagcct c

51

<210> 515

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (516 is other entry)

<221> misc\_feature  
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<223> Accession number cg44931528

<400> 515  
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<210> 516  
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<221> misc\_feature  
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<210> 517  
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gcgcggcagc cccaggtcc cggggggcct cgtcacaggc tgtaggccgt g 51

<210> 518  
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51

<210> 520  
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51

<210> 521  
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attcttggca gatgctgcag ataacgtgga gagcatacga aaggcacatg t

51

<210> 522  
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<210> 523  
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<210> 524  
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<210> 525  
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<400> 525  
taacgtggag agcatacgaa aggcacatgt ttgaaccaat agtgacatac a 51

<210> 526  
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<400> 526  
taacgtggag agcatacgaa aggcacatgt ttgaaccaat agtgacatac a 51

<210> 527  
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<400> 527  
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<210> 528  
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<210> 529  
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<210> 530  
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<210> 531  
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<210> 532  
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<221> misc\_feature  
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<400> 532  
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<210> 533  
<211> 51  
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<220>  
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<400> 533  
tgtttgaacc aatagtgaca tacaggtgct aagttctgca gtaggggaag g 51

<210> 534  
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<220>  
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<221> misc\_feature  
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<400> 534  
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<210> 535  
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tgacatacag gtgctaagtt ctgcagtagg ggaagggcag agagccatgg a 51

<210> 536  
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tgacatacag gtgctaagtt ctgcattagg ggaagggcag agagccatgg a 51

<210> 537  
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<220>  
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<210> 538  
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<221> misc\_feature  
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<210> 539

<211> 51  
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<400> 539  
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<210> 540  
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<400> 540  
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51

<210> 541  
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<210> 542  
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<221> misc\_feature  
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tcctggcacc catggcagag ttgagcgatc cagtctttct gtctcctctg g 51

<210> 543  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44932430

<400> 543  
cagatctggg aatgtccagt tgggggaggg ggctgacaat gatcatgacc t 51

<210> 544  
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<220>  
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<221> misc\_feature  
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<400> 544  
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<210> 545  
<211> 51  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg44932719



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taggccttgt tcctcttcca gggaaaaaaaa gccaaatcct tatcaaggaa a 51

<210> 546  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> Accession number cg44932719

<400> 546  
taggccttgt tcctcttcca gggaagaaaa gccaaatcct tatcaaggaa a 51

<210> 547  
<211> 51  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg44938377

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<210> 548  
<211> 51  
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<220>  
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<223> Accession number cg44938377

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<210> 549  
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<212> DNA  
<213> Homo sapiens

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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44938377

<400> 549  
actcagagcc ggggggcacc agtgcagtga ctgcggattc atgggaaatg a 51

<210> 550  
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<220>  
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actcagagcc ggggggcacc agtgcggtga ctgcggattc atgggaaatg a 51

<210> 551  
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<220>  
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<210> 552  
<211> 51  
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<222> (0)...(0)

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51

<210> 553

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (554 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44938869

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51

<210> 554

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44938869

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<210> 555

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938869

<400> 555
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<210> 556
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<212> DNA
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<220>
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<223> 2 of 2 allelic variants (555 is other entry)

<221> misc_feature
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<221> misc_feature
<222> (0)...(0)
<223> Accession number cg44938869

<400> 556
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<210> 557
<211> 51
<212> DNA
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<220>
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44938869

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taaaaatgat gcaaaaaaaaa aaaaatcagg gttgtttgac accttttttc

50

<210> 559

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (560 is other entry)

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<223> Accession number cg44938869

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51

<210> 560

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (559 is other entry)

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<223> Accession number cg44938869

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51

<210> 561

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<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (562 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44939935

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<210> 562  
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<212> DNA  
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<220>  
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acagtgtggc ctcacaggta tggcaacgga agcagctccg gtggaagaaa t 51

<210> 563  
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<221> misc\_feature  
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<210> 564  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<210> 565  
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<212> DNA

<213> Homo sapiens

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<221> misc\_feature

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<223> 1 of 2 allelic variants (566 is other entry)

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44

<210> 566

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<212> DNA

<213> Homo sapiens

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<223> Accession number cg44939948

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ntgcagcgga ggagagagtg ggggccaccg tggggcggtc gcac

44

<210> 567

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (568 is other entry)

<221> misc\_feature

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<223> Accession number cg44963511

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51

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<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (567 is other entry)

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<210> 569  
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<212> DNA  
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<221> misc\_feature  
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<210> 570  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg44963787

<400> 570  
tggtaagggg atttttgtat aagtcattag ttgttgaatc attttctcat 50

<210> 571  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature



<222> (26)...(0)  
<223> 1 of 2 allelic variants (572 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44963787

<400> 571  
caggattcta tgaattaatt tttaagtagc ttagtatcat tcaatagtat t 51

<210> 572  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (571 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44963787

<400> 572  
caggattcta tgaattaatt tttaactagc ttagtatcat tcaatagtat t 51

<210> 573  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (574 is other entry)

<221> misc\_feature  
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<400> 573  
aataccaggt tacttatact acctattcat gtatgacatt tgtgttagta t 51

<210> 574  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 574  
aataccaggt tacttatact acctactcat gtatgacatt tgtgttagta t 51

<210> 575  
<211> 51  
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<221> misc\_feature  
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<223> Accession number cg44963787

<400> 575  
tcataaaagg ggctatgagc tagacctgca gattaacacg cagatgtggc c 51

<210> 576  
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<212> DNA  
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<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44963787

<400> 576  
tcataaaagg ggctatgagc tagactgcag attaacacgc agatgtggcc 50

<210> 577  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (578 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44963787

<400> 577

cacgcagatg tggccttaaa aaaaaatcag ttaatctggg atccagagaa g

51

<210> 578

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44963787

<400> 578

cacgcagatg tggccttaaa aaaaatcagt taatctggga tccagagaag

50

<210> 579

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (580 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44964193

<400> 579

ccttagcctt ccataatgga gaagtcgggc aggggatgtc tgcatgcaat a

51

<210> 580

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (579 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44964193

<400> 580

ccttagcctt ccataatgga gaagttgggc aggggatgtc tgcatgcaat a

51

<210> 581  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (582 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44964193

<400> 581  
gggcagggga tgtctgcatg caatagacaa ctgaattaga aagagcagaa a

51

<210> 582  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (581 is other entry)

<221> misc\_feature  
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<223> Accession number cg44964193

<400> 582  
gggcagggga tgtctgcatg caataaacia ctgaattaga aagagcagaa a

51

<210> 583  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (584 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44964193

<400> 583  
ttagaaagag cagaaatgta aaccagcagt gcttcctat cttgggcctg g

51

<210> 584  
<211> 51  
<212> DNA  
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<220>

<221> misc\_feature  
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<223> 2 of 2 allelic variants (583 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44964193

<400> 584  
ttagaaagag cagaaatgta aaccaacagt gcttcctat cttgggctg g 51

<210> 585  
<211> 51  
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<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (586 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44965051

<400> 585  
tgtccaaca ttactggct ttgggtccag tggcacagat gcagcatcag a 51

<210> 586  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (585 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44965051

<400> 586  
tgtccaaca ttactggct ttgggccag tggcacagat gcagcatcag a 51

<210> 587  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (588 is other entry)

<221> misc\_feature  
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<223> Accession number cg44965051

<400> 587

tgggtccagt ggcacagatg cagcatcaga accctccctc ccatacctcaa g

51

<210> 588

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (587 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44965051

<400> 588

tgggtccagt ggcacagatg cagcagcaga accctccctc ccatacctcaa g

51

<210> 589

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (590 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44965597

<400> 589

cctgacctta acctatatac tgatggaagt tcatttgtgg agaattgggat a

51

<210> 590

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (589 is other entry)

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<222> (0)...(0)

<223> Accession number cg44965597

<400> 590

cctgacctta acctatatac tgatgaaagt tcatttgtgg agaattgggat a

51

<210> 591

<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (592 is other entry)

<221> misc\_feature  
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<223> Accession number cg44965597

<400> 591  
ggatacaaag ggcaggttat gccatagtta gtgatgtaac cataactgaa a

51

<210> 592  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (591 is other entry)

<221> misc\_feature  
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<223> Accession number cg44965597

<400> 592  
ggatacaaag ggcaggttat gccatgggta gtgatgtaac cataactgaa a

51

<210> 593  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (594 is other entry)

<221> misc\_feature  
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<223> Accession number cg44965597

<400> 593  
ccccagggac cagtgccag ttagcggaac tagtggcact taccgagcc t

51

<210> 594  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
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<221> misc\_feature  
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<223> Accession number cg44965597

<400> 594  
ccccaggac cagtgccag ttagcagaac tagtggcact tacccgagcc t 51

<210> 595  
<211> 45  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (20)...(0)  
<223> 1 of 2 allelic variants (596 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg5621185

<400> 595  
tcctaggatt gctagcgcag caaacgccat tgtttgagag ctgtg 45

<210> 596  
<211> 44  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 19 and 20

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg5621185

<400> 596  
tcctaggatt gctagcgcac aaacgccatt gtttgagagc ttgt 44

<210> 597  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (598 is other entry)



<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg5738781

<400> 597  
aatagaaagg tatgagtctc aggacggggt ctctgcaaag cagccatcgg c 51

<210> 598  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (597 is other entry)

<221> misc\_feature  
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<223> Accession number cg5738781

<400> 598  
aatagaaagg tatgagtctc aggactgggt ctctgcaaag cagccatcgg c 51

<210> 599  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (600 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg6370826

<400> 599  
gttctcttct tttgtctttt ttttttcttt agagacgggg tctagctatg t 51

<210> 600  
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<220>  
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<221> misc\_feature  
<222> (25)...(26)  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg6370826

<400> 600

gttctcttct tttgtctttt tttttcttta gagacggggt ctagctatgt

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<210> 601

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 1 of 2 allelic variants (602 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg6586279

<400> 601

gcgggaatgt gactgagggg cagggcccag cggctccctg cagccatcag g

51

<210> 602

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (601 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg6586279

<400> 602

gcgggaatgt gactgagggg cagggccagc ggctccctgc agccatcagg

50

<210> 603

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (604 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg8754307

<400> 603  
ttgtatgcta gggctttcaa ggggccttcg gagtggctgt tgattgtagc a 51

<210> 604  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (603 is other entry)

<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg8754307

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ttgtatgcta gggctttcaa ggggccttcg agtggctgtt gattgtagca 50

<210> 605  
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<220>  
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<223> 1 of 2 allelic variants (606 is other entry)

<221> misc\_feature  
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<400> 605  
aaaacatggt atatctcgat ttatcacata aagatccaca tgaattagac g 51

<210> 606  
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<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
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<221> misc\_feature  
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<223> Accession number cg9886159

<400> 606

aaaacatggg atatctcgat ttatctcata aagatccaca tgaattagac g 51

<210> 607  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (608 is other entry)

<221> misc\_feature  
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<223> Accession number cg9886159

<400> 607  
ataaagatcc acatgaatta gacgtaaaac taggtggtat cattgaaatc t 51

<210> 608  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (607 is other entry)

<221> misc\_feature  
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<223> Accession number cg9886159

<400> 608  
ataaagatcc acatgaatta gacgttaaac taggtggtat cattgaaatc t 51

<210> 609  
<211> 51  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (610 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20595730

<400> 609  
aaattgaaca gagagccaaa taaacatgag aaactttatt tctccaaaga c 51

<210> 610  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (609 is other entry)

<221> misc\_feature  
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<400> 610  
aaattgaaca gagagccaaa taaacctgag aaactttatt tctccaaaga c 51

<210> 611  
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<220>  
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<221> misc\_feature  
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<400> 611  
agcaaggtgg acctggtgcc tgggcacacc atgccatgct ctggagccct g 51

<210> 612  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg20611295

<400> 612  
agcaaggtgg acctggtgcc tgggccacca tgccatgctc tggagccctg 50

<210> 613  
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<220>

<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20614578

<400> 613  
attctctggg ttggagcgtg atggcgatcat ctatgggttg ggcacactgg a 51

<210> 614  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (613 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20614578

<400> 614  
attctctggg ttggagcgtg atggcatcat ctatgggttg ggcacactgg a 51

<210> 615  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (616 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20614578

<400> 615  
ggagcgtgat ggcgtcatct atgggtgggg cacactggac gacaagaact c 51

<210> 616  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (615 is other entry)

<221> misc\_feature  
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<223> Accession number cg20614578

<400> 616

ggagcgtgat ggcgtcatct atggtcgggg cacactggac gacaagaact c

51

<210> 617

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (618 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg20615101

<400> 617

attattaatt tgtaatcatt ttaacagcct ttcttcact gtaaaaaggg t

51

<210> 618

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (617 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg20615101

<400> 618

attattaatt tgtaatcatt ttaacggcct ttcttcact gtaaaaaggg t

51

<210> 619

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (620 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg20622181

<400> 619

ccatcttgat gaagagcgga cgtaccgga acaccacggc gacagccagg a

51

<210> 620

<211> 51  
<212> DNA  
<213> Homo sapiens  
  
<220>  
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<223> 2 of 2 allelic variants (619 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20622181  
  
<400> 620  
ccatcttgat gaagagcgga cgtacagcga acaccacggc gacagccagg a 51  
  
<210> 621  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
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<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (622 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20627797  
  
<400> 621  
ccttcgttaa aactgtcagt gtgggggata ccatcggtta cggcagaaca t 51  
  
<210> 622  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
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<223> 2 of 2 allelic variants (621 is other entry)  
  
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<400> 622  
ccttcgttaa aactgtcagt gtgggtgata ccatcggtta cggcagaaca t 51  
  
<210> 623  
<211> 51  
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<220>  
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<223> 1 of 2 allelic variants (624 is other entry)

<221> misc\_feature  
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<223> Accession number cg20627797

<400> 623  
ccatcggcta cggcagaaca tggacagcca gcgaaacgac aaaaatcgcc a 51

<210> 624  
<211> 51  
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<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (623 is other entry)

<221> misc\_feature  
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<400> 624  
ccatcggcta cggcagaaca tggaccgcca gcgaaacgac aaaaatcgcc a 51

<210> 625  
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<210> 626  
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<210> 627  
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<221> misc\_feature  
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gggcgatttc agtggcatcg gacttcgatg tgccctgcgc ccacaggggt a 51

<210> 628  
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<210> 629  
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<210> 630  
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<210> 631  
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<210> 632  
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<400> 632  
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<223> Accession number cg20631839

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51

<210> 634

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg20631839

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<223> Accession number cg20635329

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<210> 636

<211> 51

<212> DNA

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<223> Accession number cg20635329

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<210> 637  
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<210> 638  
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<210> 639  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20636603

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gctgtaggca caatccatgg cttttcactt gaagccaatg tggcctctga a 51

<210> 640  
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<220>  
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<223> Accession number cg20636603

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gctgtaggca caatccatgg ctttttactt gaagccaatg tggcctctga a 51

<210> 641  
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<223> 1 of 2 allelic variants (642 is other entry)

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<210> 642  
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<221> misc\_feature  
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<400> 642  
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<210> 643

<211> 51  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20705188

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<210> 644  
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<221> misc\_feature  
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<400> 644  
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<220>  
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<210> 646  
<211> 51  
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<213> Homo sapiens

<220>  
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<400> 646  
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<210> 647  
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<221> misc\_feature  
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<210> 648  
<211> 51  
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<210> 649  
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<221> misc\_feature  
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<400> 649  
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<210> 650  
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<221> misc\_feature  
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<210> 651  
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<210> 652  
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<222> (0)...(0)  
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<210> 653  
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<221> misc\_feature  
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gcccgcaacg tgtaggtcg ttggtatttg tgacttgtag tcggcgcgag c 51

<210> 654  
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<210> 655  
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<400> 655  
acgtgttagg tcgttggtat ttgtgacttg tgctcggcgc gagcaaacct c 51

<210> 656  
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<210> 657  
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<210> 658  
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<400> 658  
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<210> 659  
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<210> 660  
<211> 51  
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<220>  
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<400> 660  
ggatattgtg acttgtgctc ggcgcaagca aacctcctgc caggatgacg t 51

<210> 661  
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<221> misc\_feature  
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tatttgtgac ttgtgctcgg cgcgagcaaa cctcctgccca ggatgacgtg c 51

<210> 662  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg20721343

<400> 662

tatttgtagac ttgtgctcgg cgcgacaaac ctctgccag gatgacgtgc

50

<210> 663

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (664 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg20721343

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ggatgacgtg ctcagcacca acacttctca cggtcgtcac cagctccgat g

51

<210> 664

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<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (663 is other entry)

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<223> Accession number cg20721343

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ggatgacgtg ctcagcacca acactcctca cggtcgtcac cagctccgat g

51

<210> 665

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (666 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg20723457

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<210> 666  
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<400> 666  
ctttgaaaat cacacacaac ccattcgggt tttctgctat ggaaaggctc t 51

<210> 667  
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<221> misc\_feature  
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<223> Accession number cg20724478

<400> 667  
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<210> 668  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 668  
gaggctgggg agctcggcct ggctgagata cgcatgtcg tcaacgccag c 51

<210> 669  
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<213> Homo sapiens

<220>  
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ctggggagct cggcctggct gggatacgcg atgtcgtaa cgccagcccg t 51

<210> 670  
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ctggggagct cggcctggct gggattcgcg atgtcgtaa cgccagcccg t 51

<210> 671  
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<221> misc\_feature  
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aagacgtagc cggggtggga tgtgacggcc tgagcgctgt ctgggcgatt t 51

<210> 672  
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<220>  
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<221> misc\_feature  
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<400> 672  
aagacgtagc ccggtggga tgtgatggcc tgagcgtcgt ctcggcgatt t 51

<210> 673  
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<221> misc\_feature  
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<400> 673  
gaggggtgcc cctcatcatt gatgatcgcg tacatctcgt tgccgaaatt g 51

<210> 674  
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<220>  
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<400> 674  
gaggggtgcc cctcatcatt gatgaccgcg tacatctcgt tgccgaaatt g 51

<210> 675  
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<220>  
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<221> misc\_feature  
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<400> 675



cacgtgcaca tctgcggtga ggttgagggc tgcagtgata ttgaaagtct c 51

<210> 676  
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<220>  
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<221> misc\_feature  
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<210> 677  
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<223> Accession number cg20728358

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<222> (0)...(0)  
<223> Accession number cg20728358

<400> 678  
gatgaaaccc cgtctctact aaaaacacaa aaattagccg ggtgtgatgg c 51

<210> 679  
<211> 36  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (680 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20730743

<400> 679  
acgcgtactg gcggatctca gtacgataac ccacca 36

<210> 680  
<211> 36  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (11)...(0)  
<223> 2 of 2 allelic variants (679 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20730743

<400> 680  
acgcgtactg acggatctca gtacgataac ccacca 36

<210> 681  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (682 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20730927

<400> 681  
atctgaacat ctttttatcg actactggcc ccagtgaacc tatgcaacgt c 51

<210> 682  
<211> 51  
<212> DNA  
<213> Homo sapiens

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<223> 2 of 2 allelic variants (681 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 682  
atctgaacat ctttttatcg actaccggcc ccagtgaacc tatgcaacgt c 51

<210> 683  
<211> 51  
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<220>  
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<223> 1 of 2 allelic variants (684 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20738127

<400> 683  
tcgatgtcga agttcgcttc gatgggcccg gaggatagcg cgtcaggtgg c 51

<210> 684  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (683 is other entry)

<221> misc\_feature  
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<400> 684  
tcgatgtcga agttcgcttc gatggccccg gaggatagcg cgtcaggtgg c 51

<210> 685  
<211> 51  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20744814

<400> 685  
ccatggccac ccacgaagct ctccctgcc cctccgtcgc ccaactcctg g 51

<210> 686  
<211> 51  
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<213> Homo sapiens  
  
<220>  
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<223> 2 of 2 allelic variants (685 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20744814  
  
<400> 686  
ccatggccac ccacgaagct ctccccgcc cctcgcgcg ccaactcctg g 51  
  
<210> 687  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
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<223> 1 of 2 allelic variants (688 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20744814  
  
<400> 687  
gaggggcacc cgggtgctgc tggccatggc caccacgaa gctctccctg c 51  
  
<210> 688  
<211> 51  
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<223> 2 of 2 allelic variants (687 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20744814  
  
<400> 688  
gaggggcacc cgggtgctgc tggcgtggc caccacgaa gctctccctg c 51  
  
<210> 689  
<211> 46  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (21)...(0)  
<223> 1 of 2 allelic variants (690 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20745811

<400> 689  
nacgcgtggg gcatgtcaga gcttcagatg tgcattgcga acatgc

46

<210> 690  
<211> 46  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (689 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg20745811

<400> 690  
nacgcgtggg gcatgtcaga acttcagatg tgcattgcga acatgc

46

<210> 691  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (692 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21132570

<400> 691  
gtatgtacga gtgtgcacgt gtgtgcgtgt gcacagaggg tgtgggtgcca g

51

<210> 692  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (691 is other entry)

<221> misc\_feature

<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21132570

<400> 692  
gtatgtacga gtgtgcacgt gtgtggtgtg cacagagggt gtggtgccag 50

<210> 693  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (694 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21132570

<400> 693  
cgagtgtgca cgtgtgtgcg tgtgcacaga ggtgtggtg ccagcttgag t 51

<210> 694  
<211> 50  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (693 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21132570

<400> 694  
cgagtgtgca cgtgtgtgcg tgtgccagag ggtgtggtgc cagcttgagt 50

<210> 695  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (696 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21147609

<400> 695  
agtgcagagc caggatccac ctgagtcccc cggctggctc cagatccac a 51

<210> 696  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (695 is other entry)

<221> misc\_feature  
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<223> Accession number cg21147609

<400> 696  
agtgcagagc caggatccac ctgagcccc cggctggctc cagatccac a 51

<210> 697  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (698 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21147771

<400> 697  
gactggctta ttccacttag cataatgtcc tcaaggtgtg ttcacccatg t 51

<210> 698  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (697 is other entry)

<221> misc\_feature  
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<400> 698

gactggctta ttccacttag cataacgtcc tcaaggtgtg ttcacccatg t 51

<210> 699

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (700 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21147771

<400> 699

gtttgacaga gtatcactct gtcacccagg ctggagtgca gtgatgcaat c 51

<210> 700

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (699 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21147771

<400> 700

gtttgacaga gtatcactct gtcactcagg ctggagtgca gtgatgcaat c 51

<210> 701

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (702 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21147771

<400> 701

gctggagtgca agtgatgcaa tctcgggtca ctgcaacctc cgctcccag c 51

<210> 702

<211> 51

<212> DNA

<213> Homo sapiens



<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (701 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21147771

<400> 702  
gctggagtgc agtgatgcaa tctcgactca ctgcaacctc cgctcccag c 51

<210> 703  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (704 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21148047

<400> 703  
tgcttatatt cctgttggtg ggaatataaa accgtacatc tagtatggaa a 51

<210> 704  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (703 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21148047

<400> 704  
tgcttatatt cctgttggtg ggaatgtaaa accgtacatc tagtatggaa a 51

<210> 705  
<211> 51  
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<220>  
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<221> misc\_feature  
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<400> 705  
attgagggat gaatggaaaa acaaaatctg acatatacat acatacagtg g 51

<210> 706  
<211> 51  
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<220>  
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<221> misc\_feature  
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<400> 706  
attgagggat gaatggaaaa acaaagtctg acatatacat acatacagtg g 51

<210> 707  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21148047

<400> 707  
catatagaca tatgctataa catggatgca ccttgagtac attatgctag g 51

<210> 708  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
<222> (0)...(0)  
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<400> 708  
catatagaca tatgctataa catggctgca ccttgagtac attatgctag g 51

<210> 709  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (710 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21148047

<400> 709  
ggatgcacct tgagtacatt atgctagggtg aaataagcct gtcacaaaaa c 51

<210> 710  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (709 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21148047

<400> 710  
ggatgcacct tgagtacatt atgctgggtg aaataagcct gtcacaaaaa c 51

<210> 711  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (712 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21148047

<400> 711  
tgagtacatt atgctagggtg aaataagcct gtcacaaaaa caaatactgc a 51

<210> 712  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (711 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21148047

<400> 712  
tgagtacatt atgctaggtag aaataggcct gtcacaaaaa caaatactgc a 51

<210> 713  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (714 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21148047

<400> 713  
aaacaaatac tgcattgattc cattttaaag aggggcctag aatattcaac t 51

<210> 714  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (713 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 714  
aaacaaatac tgcattgattc catttgaatg aggggcctag aatattcaac t 51

<210> 715  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (716 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg21148047

<400> 715  
aacaaatact gcatgattcc atttaaata ggggcctaga atattcaact t 51

<210> 716  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (715 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 716  
aacaaatact gcatgattcc atttagatga ggggcctaga atattcaact t 51

<210> 717  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (718 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21150410

<400> 717  
ggcggaggtt tcagagtaga aggtgatgac agctccagct cccctctgac g 51

<210> 718  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (717 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21150410

<400> 718  
ggcggaggtt tcagagtaga aggtggtgac agctccagct cccctctgac g 51

<210> 719  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (720 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21150410

<400> 719  
gaataagaag atgaagtttg cagtcgaatt catgttctcc taccctgct c 51

<210> 720  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (719 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21150410

<400> 720  
gaataagaag atgaagtttg cagtcaaatt catgttctcc taccctgct c 51

<210> 721  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (722 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21405503

<400> 721  
gaaagacttc tagttcacag gggctgtatc tgaaccctaa aacaggccca g 51

<210> 722  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>

<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (721 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21405503

<400> 722  
gaaagacttc tagttcacag gggctctatc tgaaccctaa aacaggccca g 51

<210> 723  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (724 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21415668

<400> 723  
ggactggtca gggaggagtt agggcaggag gactggtcag ggaggagtta g 51

<210> 724  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (723 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21415668

<400> 724  
ggactggtca gggaggagtt agggctggag gactggtcag ggaggagtta g 51

<210> 725  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (726 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg21415668

<400> 725

ggactggtca gggaggagtt agggcaggag gactggtcag ggaggagtta g

51

<210> 726

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (725 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21415668

<400> 726

ggactggtca gggaggagtt agggctggag gactggtcag ggaggagtta g

51

<210> 727

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (728 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21417734

<400> 727

tcttgccgt tctcgacagg agcgcacat ggaccagccc agcaatctgt t

51

<210> 728

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (727 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21417734



<400> 728  
tcctggccgt tctcgacagg agcgctcatg gaccagccca gcaatctgtt 50

<210> 729  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (730 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21424662

<400> 729  
tgaggaagag gaaatacaga actcagctgt cccgggggtg cgcgctgtg t 51

<210> 730  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (729 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21424662

<400> 730  
tgaggaagag gaaatacaga actcacctgt cccgggggtg cgcgctgtg t 51

<210> 731  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (732 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21424662

<400> 731  
gtgtgtgtgc gcgagcgcg gcgaggcggc gtgtgtgtgt gtgtgtgtgt g 51

<210> 732  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (731 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21424662

<400> 732  
gtgctgtgcc gcgagcgcg gcgagacggc gtgtgtgtgt gtgtgtgtgt g 51

<210> 733  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg21424662

<400> 733  
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<210> 734  
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<221> misc\_feature  
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<223> Accession number cg21424662

<400> 734  
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<210> 735  
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<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (736 is other entry)

<221> misc\_feature  
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<210> 736  
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<212> DNA  
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<220>  
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<210> 737  
<211> 51  
<212> DNA  
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<221> misc\_feature  
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<400> 737  
ggaccgttcg cgctgacctg ggctcgttgg agggcattat gcctccggcg g 51

<210> 738  
<211> 51  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21424863

<400> 738

ggaccgttcg cgtcgacctg ggctcattgg agggcattat gcctccggcg g

51

<210> 739

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (740 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21424863

<400> 739

tcgttgagg gcattatgcc tccggcggaa caggttcccg gggagaaata t

51

<210> 740

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21424863

<400> 740

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50

<210> 741

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (742 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21424863

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<210> 742  
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<210> 743  
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<221> misc\_feature  
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ggacgagcag aaatacggtc atttttccgc cgttgagggt gacgtcatca c 51

<210> 744  
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<221> misc\_feature  
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<400> 744  
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<210> 745  
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<221> misc\_feature  
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<210> 746  
<211> 51  
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<221> misc\_feature  
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<400> 746  
agcagaaata cggtcatttt tccgccgttg agggtgacgt catcacgga g 51

<210> 747  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg21424863

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aatacggtca tttttccgcc gttgagggtg acgtcatcac cggagtcgtc c 51

<210> 748  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (747 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21424863

<400> 748

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51

<210> 749

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (750 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21425684

<400> 749

tgcacctgac gcggttcgac gtgcagatcg aggccttcga agagcccctc c

51

<210> 750

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (749 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21425684

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tgcacctgac gcggttcgac gtgcatatcg aggccttcga agagcccctc c

51

<210> 751

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (752 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21425684

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agaaggcatc cgtgaggatc cgcacagcca gggccagggc gatttccttg a 51

<210> 752  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (751 is other entry)

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<400> 752  
agaaggcatc cgtgaggatc cgcacggcca gggccagggc gatttccttg a 51

<210> 753  
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<221> misc\_feature  
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ccccagaaga gggagggcgc tctctgccca ggagacctgc tgtgctccca t 51

<210> 754  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 754  
ccccagaaga gggagggcgc tctcttccca ggagacctgc tgtgctccca t 51

<210> 755  
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<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (756 is other entry)

<221> misc\_feature  
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<223> Accession number cg21428753

<400> 755  
ccttcctct gtacctgtgt cctgacccc tttcttata aggacacgg t 51

<210> 756  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (755 is other entry)

<221> misc\_feature  
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<400> 756  
ccttcctct gtacctgtgt cctgaacccc tttcttata aggacacgg t 51

<210> 757  
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<212> DNA  
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<220>  
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<222> (26)...(0)  
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<221> misc\_feature  
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<400> 757  
catcagaggt gaaaacgatg agcggggtgc tcggacgcag acgagcgata c 51

<210> 758  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (757 is other entry)

<221> misc\_feature  
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<223> Accession number cg21428762

<400> 758  
catcagaggt gaaaacgatg agcgggtgtgc tcggacgcag acgagcgata c 51

<210> 759  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (760 is other entry)

<221> misc\_feature  
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<223> Accession number cg21428762

<400> 759  
acaccggggt aacgacggcg tgagcgcccc agaccaggc gagggctcttg g 51

<210> 760  
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<400> 760  
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<210> 761  
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<220>  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21433543

<400> 761

tacgcctccc tcaccactcc gacgcgtacc ttcgtcgtcg ccgtgacagc a

51

<210> 762

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (761 is other entry)

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<222> (0)...(0)

<223> Accession number cg21433543

<400> 762

tacgcctccc tcaccactcc gacgcatacc ttcgtcgtcg ccgtgacagc a

51

<210> 763

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (764 is other entry)

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<223> Accession number cg21433543

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tccgacgcgt accttcgtcg tcgccgtgac agcagccgta tgcggggccg c

51

<210> 764

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (763 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21433543

<400> 764

tccgacgcgt accttcgtcg tcgccatgac agcagccgta tgcggggccg c

51

<210> 765  
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<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (766 is other entry)

<221> misc\_feature  
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<223> Accession number cg21433543

<400> 765  
cactgaagtt atggcgtcgc tgcgtagccg aggctgggggt agcgctcctg g 51

<210> 766  
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<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (765 is other entry)

<221> misc\_feature  
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<223> Accession number cg21433543

<400> 766  
cactgaagtt atggcgtcgc tgcgtagccg aggctgggggt agcgctcctg g 51

<210> 767  
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<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (768 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21435343

<400> 767  
cggggcctct ggctggcag ccgcaggacc caatggatcg ggcgctcacg c 51

<210> 768  
<211> 50  
<212> DNA  
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<220>

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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21435343

<400> 768  
cggggcctct ggccctggcag ccgcagaccc aatggatcgg gcgctcacgc 50

<210> 769  
<211> 51  
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<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (770 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21435589

<400> 769  
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<210> 770  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (769 is other entry)

<221> misc\_feature  
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<223> Accession number cg21435589

<400> 770  
tcattttgtg ccaagataca ctgtcagtgct ctgatccgga atgggtctgtg t 51

<210> 771  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (772 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21628871

<400> 771

gcccggaccc tgtaccgcga ccaggacaca gcccatcact aatcaatgat a

51

<210> 772

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (771 is other entry)

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<222> (0)...(0)

<223> Accession number cg21628871

<400> 772

gcccggaccc tgtaccgcga ccagggcaca gcccatcact aatcaatgat a

51

<210> 773

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (774 is other entry)

<221> misc\_feature

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<223> Accession number cg21628871

<400> 773

ggacacagcc catcactaat caatgatatt tccataaacc aaagagaatt c

51

<210> 774

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (773 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21628871

<400> 774  
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<210> 775  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (776 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21632268

<400> 775  
aagaacacccc gtgacaaaag aaggagggcc ggcagaatga cccgccggcc c 51

<210> 776  
<211> 50  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (775 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21632268

<400> 776  
aagaacacccc gtgacaaaag aaggaggccg gcagaatgac cccgccggccc 50

<210> 777  
<211> 51  
<212> DNA  
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<221> misc\_feature  
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<223> Accession number cg21632268

<400> 777  
gacggtcgtc acttctcctc tttgggcagc cgccactggt cgtgctcggt g 51

<210> 778  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg21632268

<400> 778  
gacggtcgtc acttctcctc ttggcagcc gccactggtc gtgctcggtg

50

<210> 779  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (780 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21632268

<400> 779  
gcggacgcgg gccgtgataa tcagggccgt aggctcccg agcggggcga c

51

<210> 780  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (779 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21632268



<400> 780  
gcggaacgcgg gccgtgataa tcaggccgta ggctcccga gcggggcgac 50

<210> 781  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (782 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21632288

<400> 781  
gtgtgagggg cgcggcgcc cctagccggc cctgcgccgg ggtctcagag g 51

<210> 782  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (781 is other entry)

<221> misc\_feature  
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<223> Accession number cg21632288

<400> 782  
gtgtgagggg cgcggcgcc cctagccggc cctgcgccgg ggtctcagag g 51

<210> 783  
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<220>  
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<221> misc\_feature  
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<400> 783  
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<210> 784  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<221> misc\_feature  
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<400> 784  
gccgggggtct cagagggccg gccgcgggg ggcgcgcgg ggccaggact 50

<210> 785  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (786 is other entry)

<221> misc\_feature  
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<223> Accession number cg21632288

<400> 785  
gagggccggc ccggcggggg gcgccgcggg gccaggactg cgctcaggat c 51

<210> 786  
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<220>  
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<223> 2 of 2 allelic variants (785 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21632288

<400> 786  
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<210> 787

<211> 51  
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<220>  
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<221> misc\_feature  
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cctggctcag cagagccgcc ttctgtgc agaagctgat gtcgccccac c 51

<210> 788  
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<400> 788  
cctggctcag cagagccgcc ttctactgc agaagctgat gtcgccccac c 51

<210> 789  
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<221> misc\_feature  
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<223> Accession number cg21638303

<400> 789  
caagcctggt atacaaccag atctcatgag aactcactat cacaaggtea g 51

<210> 790  
<211> 51  
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<210> 791  
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<223> 1 of 2 allelic variants (792 is other entry)

<221> misc\_feature  
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tgagaactca ctatcacaag gtcagcatca agaagatggt gcttaaccat t 51

<210> 792  
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<400> 793  
tcacaaggctc agcatcaaga agatggtgct taaccattgg tgaaagatcc g 51

<210> 794  
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<220>  
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tcacaaggctc agcatcaaga agatggtgct taaccattgg tgaaagatcc g 51

<210> 795  
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<221> misc\_feature  
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<223> Accession number cg21638638

<400> 795  
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<210> 796  
<211> 51  
<212> DNA  
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<220>  
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<223> Accession number cg21638638

<400> 796  
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<210> 797  
<211> 51

<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (798 is other entry)

<221> misc\_feature  
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<223> Accession number cg21639240

<400> 797  
ttgccacggtt gcctaggctg gtctcaaact cctgggctca gatgatccac c 51

<210> 798  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 798  
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<210> 799  
<211> 51  
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<220>  
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<223> 1 of 2 allelic variants (800 is other entry)

<221> misc\_feature  
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<223> Accession number cg21639652

<400> 799  
aaaacccatg cactcctgtg ggattgcccc tgagctccac agtctctccc c 51

<210> 800  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (799 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21639652

<400> 800

aaaacccatg cactcctgtg ggattacccc tgagctccac agtctctccc c

51

<210> 801

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (802 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21640260

<400> 801

tgtcaccag gctgaactgc agtgggtgtga tcttggtca ctgcaacctc c

51

<210> 802

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (801 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21640260

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tgtcaccag gctgaactgc agtggcgtga tcttggtca ctgcaacctc c

51

<210> 803

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (804 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21640260

<400> 803  
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<210> 804  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 804  
tggctcactg caacctccac ctcccgggtt caagcaattc tctgcctca g 51

<210> 805  
<211> 51  
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<220>  
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<221> misc\_feature  
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caacctccac ctcccaggtt caagcaattc tctgcctca gctcagcct c 51

<210> 806  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 806  
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<210> 807  
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<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (808 is other entry)

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<223> Accession number cg21642593

<400> 807

cggccacccc cgaccagcc cgcacgcca gggcgtagcc atcggtcatc g

51

<210> 808

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg21642593

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cggccacccc cgaccagcc cgcacaccca gggcgtagcc atcggtcatc g

51

<210> 809

<211> 51

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<223> 1 of 2 allelic variants (810 is other entry)

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<222> (0)...(0)

<223> Accession number cg21643872

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<210> 810

<211> 51

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<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (809 is other entry)

<221> misc\_feature  
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<223> Accession number cg21643872

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ccgaagaccc agccaagccg tccaaaatct tcgctcccag tggctcatg c 51

<210> 811  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg21646394

<400> 811  
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<210> 812  
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<221> misc\_feature  
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<223> Accession number cg21646394

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<210> 813  
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<221> misc\_feature  
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<400> 813

gcatccccgc acagcacgtg gtgtgtggac atgccacagc atccgcggga g

51

<210> 814

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (813 is other entry)

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<223> Accession number cg21651520

<400> 814

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51

<210> 815

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (816 is other entry)

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<223> Accession number cg21652256

<400> 815

actgcagcgt gagccctggg acgcagtcga agcagagcaa agtctcccc g

51

<210> 816

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (815 is other entry)

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<223> Accession number cg21652256

<400> 816

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51

<210> 817

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature  
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<223> Accession number cg21655657

<400> 817  
caacatacat ggcgtttgcg tcacagttgg agtcagatgt gagcccgagg g 51

<210> 818  
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<220>  
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<221> misc\_feature  
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<400> 818  
caacatacat ggcgtttgcg tcacaattgg agtcagatgt gagcccgagg g 51

<210> 819  
<211> 51  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (820 is other entry)

<221> misc\_feature  
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<223> Accession number cg21656849

<400> 819  
caccagaac cacggattac gcaacgcacg ctgccaccag ggacgacgc c 51

<210> 820  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (819 is other entry)

<221> misc\_feature  
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<400> 820  
caccagaac cacggattac gcaacacacg ctgccaccag ggacgacg c 51

<210> 821  
<211> 51  
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<220>  
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<223> 1 of 2 allelic variants (822 is other entry)

<221> misc\_feature  
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<223> Accession number cg21656849

<400> 821  
aggactgggtt ggtgatcccc gggatgacac cttctgacc ttgctgctcg a 51

<210> 822  
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<400> 822  
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<210> 823  
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<220>  
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<210> 824  
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<400> 824  
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<210> 825  
<211> 51  
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<220>  
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<223> 1 of 2 allelic variants (826 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21659091

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<210> 826  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (825 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21659091

<400> 826  
gttcaaacca aatcctgctc ctgagtagac agaaggggca ggacttccag a 51

<210> 827  
<211> 38  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (13)...(0)  
<223> 1 of 2 allelic variants (828 is other entry)

<221> misc\_feature  
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<223> Accession number cg21659216

<400> 827  
acgcgtgtgt cctgtgacta caaaacagca ctgggggtt

38

<210> 828  
<211> 38  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (13)...(0)  
<223> 2 of 2 allelic variants (827 is other entry)

<221> misc\_feature  
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<223> Accession number cg21659216

<400> 828  
acgcgtgtgt cccgtgacta caaaacagca ctgggggtt

38

<210> 829  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (830 is other entry)

<221> misc\_feature  
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<400> 829  
aaggatgctg ggacctggag tcaggcaagt tgcagccaag ctcagccttt g

51

<210> 830  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (829 is other entry)

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<222> (0)...(0)  
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<400> 830  
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<210> 831  
<211> 51  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (832 is other entry)

<221> misc\_feature  
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<223> Accession number cg21659349

<400> 831  
acattgcct caatggagac ccggtcaaac cctcccacgc cgtgaaaccc g 51

<210> 832  
<211> 51  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (831 is other entry)

<221> misc\_feature  
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<223> Accession number cg21659349

<400> 832  
acattgcct caatggagac ccggttaaac cctcccacgc cgtgaaaccc g 51

<210> 833  
<211> 51  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (834 is other entry)

<221> misc\_feature  
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<223> Accession number cg21659349

<400> 833  
ggagaccgg tcaaaccctc ccacgccgtg aaaccggcg ataccgtcac c 51



<210> 834  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (833 is other entry)

<221> misc\_feature  
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<223> Accession number cg21659349

<400> 834  
ggagaccg tcaaaccctc ccacgacgtg aaaccggcg ataccgtcac c 51

<210> 835  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (836 is other entry)

<221> misc\_feature  
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<223> Accession number cg21659349

<400> 835  
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<210> 836  
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<220>  
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<221> misc\_feature  
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<400> 836  
cgtgaaaccc ggcgataccg tcaccatcca ccccccgga tgggaccggg t 51

<210> 837  
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<220>

<221> misc\_feature  
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<221> misc\_feature  
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<400> 837  
tccacacccc cggatgggac cgggttctcc aggtcatcaa cccgatcacg a 51

<210> 838  
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tccacacccc cggatgggac cgggtcctcc aggtcatcaa cccgatcacg a 51

<210> 839  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg21660290

<400> 839  
agggtggaacg ggcactggac ctgtgcatgg cgtgcaaagg gtgcgccga g 51

<210> 840  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (839 is other entry)

<221> misc\_feature  
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<223> Accession number cg21660290

<400> 840

aggtggaacg ggcactggac ctgtgtatgg cgtgcaaagg gtgcgcccga g

51

<210> 841

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (842 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21660634

<400> 841

cccacaccag gaaacagata ccaataaggg tccacgtgac gaccggaaca t

51

<210> 842

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (841 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21660634

<400> 842

cccacaccag gaaacagata ccaatgaggg tccacgtgac gaccggaaca t

51

<210> 843

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (844 is other entry)

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21660687

<400> 843  
ctcaaccgcc tgacgcgctc gctgcccgcg cgcgccaccgt ggagttgccc 50

<210> 844  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (843 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21660687

<400> 844  
ctcaaccgcc tgacgcgctc gctgcccgcg cgcgccaccg tggagttgcc c 51

<210> 845  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (846 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21660975

<400> 845  
gcaggggcat tggggtaata gccttctagc cctttttgag ggaaacacat g 51

<210> 846  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (845 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg21660975

<400> 846  
gcaggggcat tggggtaata gccttttagc cctttttgag ggaaacacat g 51

<210> 847  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (848 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21661807

<400> 847

tgccttcagg agcagacccc cacacgtatg agccgtcgct gcgtgacgtt c

51

<210> 848

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (847 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg21661807

<400> 848

tgccttcagg agcagacccc cacacctatg agccgtcgct gcgtgacgtt c

51

<210> 849

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (850 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg23217486

<400> 849

gctatggctg tggatttcgg agtgcgggga agtgtggagg aggtgttggg g

51

<210> 850

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (849 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23217486

<400> 850  
gctatggctg tggatttcgg agtgctggga agtgaggagg aggtgttggg g 51

<210> 851  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (852 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23217486

<400> 851  
ggatttcgga gtgcggggaa gtgtggagga ggtgttgggg gctggagaga t 51

<210> 852  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (851 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23217486

<400> 852  
ggatttcgga gtgcggggaa gtgtgcagga ggtgttgggg gctggagaga t 51

<210> 853  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (854 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23295774

<400> 853

gccccctcctg agtgccaagg aggcggggcgt ctacacttgc cgtgcacaca a 51

<210> 854

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (853 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg23295774

<400> 854

gccccctcctg agtgccaagg aggcgagcgt ctacacttgc cgtgcacaca a 51

<210> 855

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (856 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg23295774

<400> 855

gccaaactcta cgtcaatacgt cgtggcggtg gcagcaaccg ggcccccaaa a 51

<210> 856

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (855 is other entry)

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<222> (0)...(0)

<223> Accession number cg23295774

<400> 856

gccaaactcta cgtcaatacgt cgtggaggtg gcagcaaccg ggcccccaaa a 51

<210> 857

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (858 is other entry)

<221> misc\_feature  
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<223> Accession number cg23298372

<400> 857  
cgcggtgatag gctcaggagc ctgcctgtgt acacagacag cacacatgac a 51

<210> 858  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (857 is other entry)

<221> misc\_feature  
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<223> Accession number cg23298372

<400> 858  
cgcggtgatag gctcaggagc ctgcccgtgt acacagacag cacacatgac a 51

<210> 859  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (860 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23298372

<400> 859  
ctgtgtacac agacagcaca catgacaggc ccgggagcct gtctgtgtac a 51

<210> 860  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (859 is other entry)



<221> misc\_feature  
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<223> Accession number cg23298372

<400> 860  
ctgtgtacac agacagcaca catgataggc ccgggagcct gtctgtgtac a 51

<210> 861  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (862 is other entry)

<221> misc\_feature  
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<223> Accession number cg23299043

<400> 861  
agtacgacat ccgacacgct tcagaccgac cagagtgaag aatttcgcgt a 51

<210> 862  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (861 is other entry)

<221> misc\_feature  
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<223> Accession number cg23299043

<400> 862  
agtacgacat ccgacacgct tcagagcgac cagagtgaag aatttcgcgt a 51

<210> 863  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (864 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg23299248

<400> 863

ccaactatta agatatatat acccctaccc cagtgaagaa caatctgcta

50

<210> 864

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (863 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg23299248

<400> 864

ccaactatta agatatatat acccctacc ccagtgaaga acaatctgct a

51

<210> 865

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (866 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg23305320

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tgctgcatac caggtgccaa atggcgctcct ataaatggaa gctcttgtgt g

51

<210> 866

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (865 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg23305320

<400> 866

tgctgcatac caggtgccaa atggcatcct ataaatggaa gctcttgtgt g

51

<210> 867

<211> 51  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (868 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23306056

<400> 867  
tccagtatga ctttatctcg attacacctg taaagacctt aagccatatt t 51

<210> 868  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (867 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23306056

<400> 868  
tccagtatga ctttatctcg attaccctgt aaagacctta agccatattt 50

<210> 869  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (870 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23306056

<400> 869  
actttatctc gattacacct gtaaagacct taagccatat ttttaaggttc t 51

<210> 870  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (869 is other entry)

<221> misc\_feature

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<223> Accession number cg23306056

<400> 870

actttatctc gattacacct gtaaatacct taagccatat ttttaagggtc t

51

<210> 871

<211> 48

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (872 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg23309108

<400> 871

acgcgtgccc gttacgttga ccaggctggt tgtaaactcc tgggctca

48

<210> 872

<211> 48

<212> DNA

<213> Homo sapiens

<220>

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<222> (23)...(0)

<223> 2 of 2 allelic variants (871 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg23309108

<400> 872

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48

<210> 873

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (874 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23309108

<400> 873  
tgggctcaag tgatccacct gcctcagcct ccaaaagtgc tgggattaca t 51

<210> 874  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (873 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg23309108

<400> 874  
tgggctcaag tgatccacct gcctcggcct ccaaaagtgc tgggattaca t 51

<210> 875  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (876 is other entry)

<221> misc\_feature  
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<223> Accession number cg23331833

<400> 875  
acagcgcgta ctttgggctc cgggattcgc tccgcgcccg cggttgtagc a 51

<210> 876  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
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<221> misc\_feature  
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<400> 876

acagcgcgta ctttgggctc cgggagtcgc tccgcgcccg cggttgtagc a

51

<210> 877

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (878 is other entry)

<221> misc\_feature

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<223> Accession number cg23332230

<400> 877

ttgtgggagt attaggggaa gttgccacta aggctggcag gtcttgaggt t

51

<210> 878

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (877 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg23332230

<400> 878

ttgtgggagt attaggggaa gttgcactaa ggctggcagg tcctggaggt

50

<210> 879

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (880 is other entry)

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<223> Accession number cg23333370

<400> 879

ttgggggctc agaggcacgg ttaacgcagc agcagcgcaa acctcacact c

51

<210> 880  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (879 is other entry)

<221> misc\_feature  
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<223> Accession number cg23333370

<400> 880  
ttgggggctc agaggcacgg ttaacacagc agcagcgcaa acctcacact c 51

<210> 881  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (882 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg24109555

<400> 881  
aatataatgg gtttatatga ctatatcaaa ggagggaaga agggccccag c 51

<210> 882  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (881 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg24109555

<400> 882  
aatataatgg gtttatatga ctatacaaaa ggagggaaga agggccccag c 51

<210> 883  
<211> 51  
<212> DNA  
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<220>

<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (884 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg24110526

<400> 883  
gcactgagac agcatcacga ggactgtgcc tgccccgcat gcctcttgcc a 51

<210> 884  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (883 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg24110526

<400> 884  
gcactgagac agcatcacga ggactatgcc tgccccgcat gcctcttgcc a 51

<210> 885  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (886 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg24113982

<400> 885  
tacttagtta tgtttttaaa cacacatctg agtcaaagc caagaaaggg a 51

<210> 886  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (885 is other entry)

<221> misc\_feature  
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<223> Accession number cg24113982

<400> 886

tacttagtta tgttttttaa cacacgtctg agtcaaagc caagaaagg a

51

<210> 887

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (888 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg24114224

<400> 887

aatgggccag gctggagcta cgttgagttt gttgagtttt ttgcttattg c

51

<210> 888

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (887 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg24114224

<400> 888

aatgggccag gctggagcta cgttgcgttt gttgagtttt ttgcttattg c

51

<210> 889

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (890 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg24114456

<400> 889

atcctgacgt gtagactcct atggagacct acttaattca caccgggtgt c

51

<210> 890

<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (889 is other entry)

<221> misc\_feature  
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<223> Accession number cg24114456

<400> 890  
atcctgacgt gtagactcct atggatacct acttaattca caccgggtgt c 51

<210> 891  
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<220>  
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<223> 1 of 2 allelic variants (892 is other entry)

<221> misc\_feature  
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<400> 891  
ttcacaccgg gtgtcctgat gtgtagaccc ctgtggagac ctacttaatt c 51

<210> 892  
<211> 51  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (891 is other entry)

<221> misc\_feature  
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<400> 892  
ttcacaccgg gtgtcctgat gtgtaaacc ctgtggagac ctacttaatt c 51

<210> 893  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 1 of 2 allelic variants (894 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg24115035

<400> 893  
gaggtgaaag ggaagaaaag ctaaggtcga ccttagaaaag cattgagtca a 51

<210> 894  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (893 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg24115035

<400> 894  
gaggtgaaag ggaagaaaag ctaagatcga ccttagaaaag cattgagtca a 51

<210> 895  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (896 is other entry)

<221> misc\_feature  
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<223> Accession number cg24115035

<400> 895  
agaactgttg ctttttgttt aaccacgtg caagtaaagt tcaataaagt t 51

<210> 896  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (895 is other entry)

<221> misc\_feature  
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<223> Accession number cg24115035

<400> 896  
agaactgttg ctttttgttt aacccccgtg caagtaaagt tcaataaagt t 51

<210> 897  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg24121961

<400> 897  
acaggccaca ccccatctc agagatggca ggcacttcac ccaaggggca g 51

<210> 898  
<211> 51  
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<221> misc\_feature  
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<223> Accession number cg24121961

<400> 898  
acaggccaca ccccatctc agagaaggca ggcacttcac ccaaggggca g 51

<210> 899  
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<220>  
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<223> 1 of 2 allelic variants (900 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg24132746

<400> 899  
cctgtggtgc tgcttctcca aatgccgcc ttggtgttt cccaggagtc a 51

<210> 900  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
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<400> 900  
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51

<210> 901  
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<221> misc\_feature  
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<400> 901  
gtgtaaagaa gtataatttc tctgccgact ccatttaatc cactgcaagg c

51

<210> 902  
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<221> misc\_feature  
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51

<210> 903  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg24144955

<400> 903

gcacgcgtgt tgtggctgga agggcgctagt gctctggagg gggaaactga g

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<210> 904

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (903 is other entry)

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<223> Accession number cg24144955

<400> 904

gcacgcgtgt tgtggctgga agggctcagt gctctggagg gggaaactga g

51

<210> 905

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (906 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg25132332

<400> 905

aagtaagtgt cttaatcagg tccaagcagt aattgagaga agagagtagc t

51

<210> 906

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (905 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg25132332

<400> 906  
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<210> 907  
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<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg25132807

<400> 907  
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<210> 908  
<211> 51  
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<221> misc\_feature  
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<210> 909  
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<223> 1 of 2 allelic variants (910 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg25147161

<400> 909  
ctgcaatatg ccaccagcgc catggcgaac cgcactctacg ctccaattcc c 51

<210> 910  
<211> 50  
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<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (909 is other entry)

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<222> (25)...(26)

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<222> (0)...(0)

<223> Accession number cg25147161

<400> 910

ctgcaatatg ccaccagcgc catgggaacc gcatctacgc tccaattccc

50

<210> 911

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (912 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg25153589

<400> 911

tcccagcact tctgggaggc caaagtggga ggatcgcttg agcccaggag t

51

<210> 912

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (911 is other entry)

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<223> Accession number cg25153589

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51

<210> 913

<211> 51

<212> DNA

<213> Homo sapiens



<220>  
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<221> misc\_feature  
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<210> 914  
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<400> 914  
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<210> 915  
<211> 51  
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<223> 1 of 2 allelic variants (916 is other entry)

<221> misc\_feature  
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<223> Accession number cg25153589

<400> 915  
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<210> 916  
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<220>  
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<223> Accession number cg25153589

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ggaggatcgc ttgagcccag gagtttgaga ccagcctggg caacatagcg a

51

<210> 917

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> Accession number cg25154211

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ggccaccag ctgcctatgc tggggacggg gccgctcagg tccccaccgg g

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<210> 918

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (917 is other entry)

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<223> Accession number cg25154211

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<210> 919

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (920 is other entry)

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<223> Accession number cg25154211

<400> 919

ccaccagct gcctatgctg gggacggggc cgctcaggtc cccaccgggc c

51

<210> 920  
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<223> 2 of 2 allelic variants (919 is other entry)  
  
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<223> Accession number cg25154211  
  
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<210> 921  
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<223> Accession number cg25154211  
  
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<210> 922  
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<221> misc\_feature  
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<223> Accession number cg25154211  
  
<400> 922  
gggccgctca ggtccccacc gggccgtgcc accggctgag gtcctctcgc 50  
  
<210> 923  
<211> 51

<212> DNA  
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<223> Accession number cg25164916

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gataataaaa cctgccccac aatttaaaaa aaaaatcat gtcagttag t 51

<210> 924  
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<223> Accession number cg25164916

<400> 924  
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<210> 925  
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<221> misc\_feature  
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<210> 926  
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<221> misc\_feature  
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<210> 927  
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<221> misc\_feature  
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tgactgtgtg tccgggccac gtgtggctat gtgtccgggc cacgtgtgac t 51

<210> 928  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg25167383

<400> 928  
tgactgtgtg tccgggccac gtgtgactat gtgtccgggc cacgtgtgac t 51

<210> 929  
<211> 51  
<212> DNA  
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<220>

<221> misc\_feature  
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<221> misc\_feature  
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<400> 929  
gaccacctcc ggtaccccggt ctgcgctgct gatatcccggt cggcctctct g 51

<210> 930  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (929 is other entry)

<221> misc\_feature  
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<400> 930  
gaccacctcc ggtaccccggt ctgcgttgct gatatcccggt cggcctctct g 51

<210> 931  
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<220>  
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<223> 1 of 2 allelic variants (932 is other entry)

<221> misc\_feature  
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<223> Accession number cg25171115

<400> 931  
gccaaagcgtt caccacgccc tgcgtgctgc aagacctgag gaacgcgcat g 51

<210> 932  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (931 is other entry)

<221> misc\_feature  
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<223> Accession number cg25171115

<400> 932

gccaaagcgtt caccacgccc tgctgtctgc aagacctgag gaacgcgcat g

51

<210> 933

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (934 is other entry)

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<222> (0)...(0)

<223> Accession number cg25171136

<400> 933

ttgcaggcca gtcggctggg ggaaacggat gccctgcagg gggacgggaa c

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<210> 934

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (933 is other entry)

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<223> Accession number cg25171136

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ttgcaggcca gtcggctggg ggaaatggat gccctgcagg gggacgggaa c

51

<210> 935

<211> 51

<212> DNA

<213> Homo sapiens

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<400> 935

gcattgtcaa cgaaacctgc gactctcttg cttctgtgc ctgcagcatg g

51

<210> 936

<211> 51  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (935 is other entry)

<221> misc\_feature  
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<400> 936  
gcattgtcaa cgaaacctgc gactcccttg ccttctgtgc ctgcagcatg g 51

<210> 937  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (938 is other entry)

<221> misc\_feature  
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<223> Accession number cg25173882

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ttgcagtcca gctttctctc accttcaccg tggtctgtgc gcaccactga g 51

<210> 938  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (937 is other entry)

<221> misc\_feature  
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<400> 938  
ttgcagtcca gctttctctc accttcaccg tggtctgtgc gcaccactga g 51

<210> 939  
<211> 51  
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<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (940 is other entry)

<221> misc\_feature  
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<400> 939  
atgctggaca cagggctcga caaacacaag agacgaccc t' 51

<210> 940  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (939 is other entry)

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<400> 940  
atgctggaca cagggctcga caaacccaag agacgaccc t 51

<210> 941  
<211> 51  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (942 is other entry)

<221> misc\_feature  
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cagtgggagc gggaagaggc cggagctcct gccccacacg tgagcaaagg g 51

<210> 942  
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<220>  
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<222> (26)...(0)  
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<221> misc\_feature  
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<223> Accession number cg25184184

<400> 942  
cagtggggagc ggggaagaggc cggagttcct gccccacacg tgagcaaagg g 51

<210> 943  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (944 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg25237193

<400> 943  
cttccaaaat gaatcccaac ttcacctgta ctagttttac agtccttaca c 51

<210> 944  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (943 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg25237193

<400> 944  
cttccaaaat gaatcccaac ttcacttgta ctagttttac agtccttaca c 51

<210> 945  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (946 is other entry)

<221> misc\_feature  
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<223> Accession number cg25239764

<400> 945  
cataacctca agaagctgtg ggagcgcaac ctccaggacg atttcctca t 51

<210> 946  
<211> 51

<212> DNA  
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<220>  
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<400> 946  
cataacctca agaagctgtg ggagcacaac ctccaggacg atttcctca t 51

<210> 947  
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<220>  
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<223> 1 of 2 allelic variants (948 is other entry)

<221> misc\_feature  
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<223> Accession number cg25244087

<400> 947  
tcgtcaccac tggcgttgtc gacgttgta aaccgaggag gttcatgcgc t 51

<210> 948  
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<210> 949  
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<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (950 is other entry)

<221> misc\_feature  
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cgatcggtcc ccttcccgct ccttaagagc cttgtaggcg caccgtctgc g 51

<210> 950  
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<220>  
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<223> Accession number cg25244087

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<210> 951  
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<210> 952  
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<221> misc\_feature  
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<210> 956  
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<223> 2 of 2 allelic variants (955 is other entry)

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<222> (0)...(0)

<223> Accession number cg25244087

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ctctcttgtg aatggggacc ggacgtccgc agcgaggaca gcggccgtcg a

51

<210> 957

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (958 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg25248402

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agaaaggcac agaggaaggg caaagcccca ggggagagaa aaccagtgac c

51

<210> 958

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (957 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg25248402

<400> 958

agaaaggcac agaggaaggg caaagcccag gggagagaaa accagtgacc

50

<210> 959

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature  
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<221> misc\_feature  
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<210> 962  
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<221> misc\_feature  
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<210> 965  
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<400> 965  
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<210> 966  
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<223> Accession number cg25257592  
  
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tgtgagcgta atgaaggtct acatcgccct ggtgaaggcc tgcaccacta g 51  
  
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tgtgagcgta atgaaggtct acatcaccct ggtgaaggcc tgcaccacta g 51  
  
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<400> 969  
aggtctacat cgccctggtg aaggcctgca ccactagcgt cggcaccatt t 51

<210> 970  
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aggtctacat cgccctggtg aaggcttgca ccactagcgt cggcaccatt t 51

<210> 971  
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<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg25261577

<400> 971  
tgataatagc gcttgccggt tagtggtaat acacagcttg aaatttggtg a 51

<210> 972  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg25261577

<400> 972

tgataatagc gcttgccggt tagtgataat acacagcttg aaatttggtg a

51

<210> 973

<211> 51

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<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (974 is other entry)

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ggggcgattt caagcagaag ctcacgacga ccttcactgc gggctccggg c

51

<210> 974

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (973 is other entry)

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<223> Accession number cg25263948

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<210> 975

<211> 51

<212> DNA

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<400> 975

cgaccttcac tgcgggctcc gggctgccc accttaccgg cgtcaagggc g

51

<210> 976

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51

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<400> 977  
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51

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<220>  
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<400> 978  
ccggtgacgc taagaagctc gtcctatgga tgtggccaga aggcttcgac a

51

<210> 979  
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<220>  
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<223> 1 of 2 allelic variants (980 is other entry)

<221> misc\_feature  
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gaaggcttcg acaagcagac gttagttgcc gtcgccaaag cgcagccgtc t 51

<210> 980  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 980  
gaaggcttcg acaagcagac gttagctgcc gtcgccaaag cgcagccgtc t 51

<210> 981  
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<212> DNA  
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<221> misc\_feature  
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<223> Accession number cg25268662

<400> 981  
cccttgagct ttgagctcag gtctagaggt gaacagagca gtcaccgggc g 51

<210> 982  
<211> 50  
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<221> misc\_feature  
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<400> 982  
cccttgagct ttgagctcag gtctaaggtg aacagagcag tcaccgggcg 50

<210> 983  
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<400> 983  
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<210> 984  
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<212> DNA  
<213> Homo sapiens

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<400> 984  
gagctttgag ctcaggtcta gaggtaaaca gagcagtcac cgggcgactc a 51

<210> 985  
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agagcagtca ccgggcgact cagacgggcc agcgctcagg gtccttggt a

51

<210> 986

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (985 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg25268662

<400> 986

agagcagtca ccgggcgact cagacgggcc agcgctcagg gtccttggt a

51

<210> 987

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (988 is other entry)

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acgggccagc gctcagggtc cttggttaata tatgcctaga gaaaggccat g

51

<210> 988

<211> 50

<212> DNA

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<223> 2 of 2 allelic variants (987 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

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<223> Accession number cg25268662

<400> 988

acgggccagc gctcagggtc cttggaatat atgcctagag aaaggccatg

50

<210> 989  
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<213> Homo sapiens  
  
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<223> Accession number cg25268662  
  
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<210> 991  
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<213> Homo sapiens  
  
<220>  
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<223> 1 of 2 allelic variants (992 is other entry)  
  
<221> misc\_feature  
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<223> Accession number cg25310296  
  
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aaactccatc tcaaaaaaaaa aaaaaaatta gtttggggat accagtaatt t 51  
  
<210> 992  
<211> 50



<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg25310296

<400> 992  
aaactccatc tcaaaaaaaaa aaaaaattag ttgggggata ccagtaattt 50

<210> 993  
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<221> misc\_feature  
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<210> 994  
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<221> misc\_feature  
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<223> Accession number cg25310296

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<210> 995  
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<220>  
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<221> misc\_feature  
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<400> 995  
cacaggcaac ccgtccagcc aagcagaagc cgtggcgtag ccgacacgcc t 51

<210> 996  
<211> 51  
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<221> misc\_feature  
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<400> 996  
cacaggcaac ccgtccagcc aagcataagc cgtggcgtag ccgacacgcc t 51

<210> 997  
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<221> misc\_feature  
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gtccagccaa gcagaagccg tggcgtagcc gacacgcctt cgacccaacc c 51

<210> 998  
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<210> 999  
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<220>  
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<223> Accession number cg25311248

<400> 999  
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<210> 1000  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<400> 1000  
tcgtgttggt cttcctcacc ctcatccat tgacgggtcat tgggtggggc a 51

<210> 1001  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1002 is other entry)

<221> misc\_feature  
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<223> Accession number cg25311248

<400> 1001  
tcaccctcat tccattgacg gtcattggtt gggccaacaa caaggacctc c 51

<210> 1002  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1002  
tcaccctcat tccattgacg gtcattggtt gggccaacaa caaggacctc c 51

<210> 1003  
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<220>  
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<221> misc\_feature  
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<400> 1003  
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<210> 1004  
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<210> 1005

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<223> Accession number cg25314764  
  
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<210> 1006  
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<212> DNA  
<213> Homo sapiens  
  
<220>  
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<223> Accession number cg25314764  
  
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tatggaagaa aagtcactcg gaagtgcctg aaatcacccc agcgctcat c 51  
  
<210> 1007  
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<223> Accession number cg25314764  
  
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aagtcactcg gaagtaccgt aaatcacccc agcgctcat cccccgaatc t 51  
  
<210> 1008  
<211> 51  
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<220>  
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<221> misc\_feature  
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<400> 1008  
aagtactcg gaagtaccgt aaatcgcccc agcgctcat cccccgaatc t 51

<210> 1009  
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<220>  
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<210> 1010  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1010  
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<210> 1011  
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<221> misc\_feature  
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<210> 1012  
<211> 51  
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<220>  
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<221> misc\_feature  
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<400> 1012  
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<210> 1013  
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<220>  
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<221> misc\_feature  
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<400> 1013  
tgttcgcat ctgctgtcgc cctgtgctt aaggcatcac ccactagac t 51

<210> 1014  
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<220>  
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<221> misc\_feature  
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<400> 1014  
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<210> 1015  
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<212> DNA  
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<210> 1016  
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<221> misc\_feature  
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<400> 1016  
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51

<210> 1017  
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<220>  
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<221> misc\_feature  
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<400> 1017  
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51

<210> 1018  
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<223> 2 of 2 allelic variants (1017 is other entry)

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<400> 1018  
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<210> 1019  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<400> 1019  
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<210> 1020  
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<221> misc\_feature  
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<400> 1020  
aggtggcagc ccgagggcc gccgtcaact tattgtgtcg tcttatggaa g 51

<210> 1021  
<211> 51  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg25314764

<400> 1021  
ggcagcccgga gggcccgccg tgaacttatt gtgtcgtctt atggaagaaa a 51

<210> 1022  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<400> 1022  
ggcagcccgga gggcccgccg tgaacatatt gtgtcgtctt atggaagaaa a 51

<210> 1023  
<211> 51  
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<220>  
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<223> 1 of 2 allelic variants (1024 is other entry)

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<223> Accession number cg27297262

<400> 1023  
cacacacaca cacacacaca cacacactca cccaagagtgt ttaaacagaa a 51

<210> 1024  
<211> 50  
<212> DNA  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg27297262

<400> 1024  
cacacacaca cacacacaca cacacctcac ccaagagtgt ttaaacagaa 50

<210> 1025  
<211> 51  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg27355682

<400> 1025  
gagacaggct tgtacataaa aaaaaatact tagattaatt cctggccctg t

51

<210> 1026  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg27355682

<400> 1026  
gagacaggct tgtacataaa aaaaatactt agattaattc ctggccctgt

50

<210> 1027  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1028 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27360908

<400> 1027  
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51

<210> 1028

<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1027 is other entry)

<221> misc\_feature  
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<223> Accession number cg27360908

<400> 1028  
gtgcggtatc cagcgtgaga agaaacgccg aaggtcacgg cgatgaccgc g

51

<210> 1029  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1030 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27364539

<400> 1029  
cgctcactgt gttgtccttc cttgggtatg tctcgatggt tcagcgatgg a

51

<210> 1030  
<211> 50  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27364539

<400> 1030  
cgctcactgt gttgtccttc cttggtatgt ctcgatgggt cagcgatgga

50

<210> 1031  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1032 is other entry)

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<222> (0)...(0)

<223> Accession number cg27369798

<400> 1031

cgacatcctg ttcacccagg gtgacatcat cagcagtaag tgttgcacag g

51

<210> 1032

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1031 is other entry)

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<223> Accession number cg27369798

<400> 1032

cgacatcctg ttcacccagg gtgacgtcat cagcagtaag tgttgcacag g

51

<210> 1033

<211> 48

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1034 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27784915

<400> 1033

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48

<210> 1034

<211> 48

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1033 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27784915

<400> 1034  
ccatagacac tcacctccga gtccgggata ttctcctcgc tgcggccg

48

<210> 1035  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg27794839

<400> 1035  
ccttcactcg caaatcgct ctctcccccac ctcccaggc ccctcctggg a

51

<210> 1036  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (1035 is other entry)

<221> misc\_feature  
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<400> 1036  
ccttcactcg caaatcgct ctctctccac ctcccaggc ccctcctggg a

51

<210> 1037  
<211> 51  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<400> 1037

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51

<210> 1038

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1037 is other entry)

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

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<222> (0)...(0)

<223> Accession number cg27802892

<400> 1038

ttgctactgc taacatcctt taggcctggg actatttcta atgcctggca

50

<210> 1039

<211> 46

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27804759

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acgcgtgccg aggcgctggg cggcggctgt gtgagttggt ggccca

46

<210> 1040

<211> 45

<212> DNA

<213> Homo sapiens

<220>

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<222> (21)...(0)

<223> 2 of 2 allelic variants (1039 is other entry)

<221> misc\_feature

<222> (20)...(21)

<223> Nucleotide deleted between bases 20 and 21

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27804759

<400> 1040  
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<210> 1041  
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<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1042 is other entry)

<221> misc\_feature  
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<400> 1041  
ctgtgtgagt tgggtggcca gacgaacagc ttgtgcgaga ctctgggcat t 51

<210> 1042  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1041 is other entry)

<221> misc\_feature  
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<400> 1042  
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<210> 1043  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1043  
ccagcaccag ttctgctggc cacgcgcctt gtcggcatgc agcacagggt c 51

<210> 1044  
<211> 50



<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 1044  
ccagcaccag ttctgctggc cagcccttg tcggcatgca gcacagggtc 50

<210> 1045  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1046 is other entry)

<221> misc\_feature  
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<223> Accession number cg27806958

<400> 1045  
agcagtggaa gggcagcggc gcacaggcat atccacagcc ccattgaccc a 51

<210> 1046  
<211> 51  
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<220>  
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<223> Accession number cg27806958

<400> 1046  
agcagtggaa gggcagcggc gcacaagcat atccacagcc ccattgaccc a 51

<210> 1047  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1048 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27807001  
  
<400> 1047  
acaatgccgt taacactgcc gctggcacca gcacggctg aaccgtgacc a 51  
  
<210> 1048  
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<212> DNA  
<213> Homo sapiens  
  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26  
  
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<223> Accession number cg27807001  
  
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<210> 1049  
<211> 51  
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<213> Homo sapiens  
  
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<223> 1 of 2 allelic variants (1050 is other entry)  
  
<221> misc\_feature  
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<223> Accession number cg27807001  
  
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<210> 1050  
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<221> misc\_feature  
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<400> 1050  
accgacttta gccttaacct tgagagccgc cttacctttg acatcgactt c 51

<210> 1051  
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<212> DNA  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<400> 1051  
cttctactgt cctcgaagtc gaagagagcc gagagttggg gacatcgggg g 51

<210> 1052  
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<400> 1052  
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<210> 1053  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg27807001

<400> 1053

ctgtcctcga agtcgaagag agccgagagt tggggacatc gggggcactg c

51

<210> 1054

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1053 is other entry)

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<222> (0)...(0)

<223> Accession number cg27807001

<400> 1054

ctgtcctcga agtcgaagag agccgggagt tggggacatc gggggcactg c

51

<210> 1055

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gagccgagag ttggggacat cgggggcact gccaaagatgc atgaccgcca g

51

<210> 1056

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1055 is other entry)

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<223> Nucleotide deleted between bases 25 and 26

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<223> Accession number cg27807001

<400> 1056  
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<210> 1057  
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<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1058 is other entry)

<221> misc\_feature  
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<223> Accession number cg27807001

<400> 1057  
gatgcatgac cgccagcgca cgttcccgag cgtacttggt caagttgtcc c 51

<210> 1058  
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<220>  
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<223> 2 of 2 allelic variants (1057 is other entry)

<221> misc\_feature  
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<223> Accession number cg27807001

<400> 1058  
gatgcatgac cgccagcgca cgttctcgag cgtacttggt caagttgtcc c 51

<210> 1059  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1060 is other entry)

<221> misc\_feature  
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<223> Accession number cg27807001

<400> 1059  
acgttccgga gcgtacttgt tcaagttgtc ccgatctgcg cgagcggcgg c 51

<210> 1060  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1059 is other entry)

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<222> (0)...(0)

<223> Accession number cg27807001

<400> 1060

acgttcccgga gcgtacttgt tcaagctgtc ccgatctgcg cgagcggcgg c

51

<210> 1061

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1062 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27825769

<400> 1061

ctgtatcttt aacagtaaaa gcgtaggaag cacatagccc caatgtattt a

51

<210> 1062

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1061 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27825769

<400> 1062

ctgtatcttt aacagtaaaa gcgtacgaag cacatagccc caatgtattt a

51

<210> 1063

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1064 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27826716

<400> 1063  
cgttggttga gaaggatgtc accaactgag gtatcgagat ctcatgccca c 51

<210> 1064  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1063 is other entry)

<221> misc\_feature  
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<223> Accession number cg27826716

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cgttggttga gaaggatgtc accaattgag gtatcgagat ctcatgccca c 51

<210> 1065  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1066 is other entry)

<221> misc\_feature  
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<223> Accession number cg27831266

<400> 1065  
taaggctgtg gaggagccag atgggggacta gcctctggac ttctgcttag g 51

<210> 1066  
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (1065 is other entry)

<221> misc\_feature  
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<400> 1066

taaggctgtg gaggagccag atgggaacta gcctctggac ttctgcttag g

51

<210> 1067

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1068 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27831595

<400> 1067

gggcctcagg gtaagctgga gttgcgggcc accgcccag gagttgagt g

51

<210> 1068

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1067 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27831595

<400> 1068

gggcctcagg gtaagctgga gttgcggcca ccgcccag agttgagtgg

50

<210> 1069

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1070 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27834324

<400> 1069

catggagtca ctcagatcac gcatcgagga aagcactaag gtaacaccca g

51



<210> 1070  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1069 is other entry)

<221> misc\_feature  
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<223> Accession number cg27834324

<400> 1070  
catggagtca ctcagatcac gcatcaagga aagcactaag gtaacaccca g

51

<210> 1071  
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<220>  
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<223> 1 of 2 allelic variants (1072 is other entry)

<221> misc\_feature  
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<223> Accession number cg27835768

<400> 1071  
cagctgttgt gtgcctggca gcgctgcttt cagccccatt cattccaac t

51

<210> 1072  
<211> 50  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27835768

<400> 1072  
cagctgttgt gtgcctggca gcgctctttc agccccattc attccaact

50

<210> 1073  
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<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1074 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27837446

<400> 1073  
tgtttgctat tttatttttt gagacaggtc tcattctgcc attcaggctg a 51

<210> 1074  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1073 is other entry)

<221> misc\_feature  
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<223> Accession number cg27837446

<400> 1074  
tgtttgctat tttatttttt gagacgggtc tcattctgcc attcaggctg a 51

<210> 1075  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1076 is other entry)

<221> misc\_feature  
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<223> Accession number cg27837446

<400> 1075  
tgtacgtgtg tgtgtgtgtg tgtgtgtaag tgtctgtgtg tacgtgtaag t 51

<210> 1076  
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<212> DNA  
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<220>  
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<221> misc\_feature

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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27837446

<400> 1076

tgtacgtgtg tgtgtgtgtg tgtgttaagt gtctgtgtgt acgtgtaagt

50

<210> 1077

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (1078 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27838870

<400> 1077

cgacaactcg atcgaccga ggcgcgacac ccgcctgccc cgtactttcc c

51

<210> 1078

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1077 is other entry)

<221> misc\_feature

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<223> Accession number cg27838870

<400> 1078

cgacaactcg atcgaccga ggcgcaacac ccgcctgccc cgtactttcc c

51

<210> 1079

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1080 is other entry)

<221> misc\_feature  
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<223> Accession number cg27838870

<400> 1079  
actttccgc catccaagt caccggtgtg tcgctcgta gcatcgctc a 51

<210> 1080  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1079 is other entry)

<221> misc\_feature  
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<223> Accession number cg27838870

<400> 1080  
actttccgc catccaagt caccggtgtg tcgctcgta gcatcgctc a 51

<210> 1081  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1082 is other entry)

<221> misc\_feature  
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<223> Accession number cg27840665

<400> 1081  
tgataggaag gatgcgcaga ttgttggtct taccgggaat atccatcggg g 51

<210> 1082  
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<221> misc\_feature  
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<400> 1082  
tgataggaag gatgcgcaga ttgttagtct taccgggaat atccatcggg g 51

<210> 1083  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg27840665

<400> 1083  
gcagattggt ggtcttacct ggaatatcca tcggggaacc ggacaacacg a

51

<210> 1084  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1083 is other entry)

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<400> 1084  
gcagattggt ggtcttacct ggaatgtcca tcggggaacc ggacaacacg a

51

<210> 1085  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg27840665

<400> 1085  
gacaacacga cgacgcggtc accgaccggc acgaaaccct tgtcgcgcag g

51

<210> 1086  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1085 is other entry)

<221> misc\_feature  
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<223> Accession number cg27840665

<400> 1086  
gacaacacga cgacgcggtc accgatcggc acgaaaccct tgtcgcgcag g 51

<210> 1087  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg27842663

<400> 1087  
ctagcctgga gtcaggagac agcaagagta ggggctgagg ttgtggggcc 50

<210> 1088  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg27842663

<400> 1088  
ctagcctgga gtcaggagac agcaaagagt aggggctgag gttgtggggc c 51

<210> 1089  
<211> 50  
<212> DNA  
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<220>  
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<222> (26)...(0)  
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<221> misc\_feature  
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<400> 1089  
ctagcctgga gtcaggagac agcaagagta ggggctgagg ttgtggggcc 50

<210> 1090  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1090  
ctagcctgga gtcaggagac agcaaagagt aggggctgag gttgtggggc c 51

<210> 1091  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1092 is other entry)

<221> misc\_feature  
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<400> 1091  
gagacagcaa gtagtaggggc tgaggttgtg gggcccaggg tcccagtgtg g 51

<210> 1092  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1091 is other entry)

<221> misc\_feature  
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<223> Accession number cg27842663

<400> 1092  
gagacagcaa gagtaggggc tgagggtgtg gggcccaggg tcccagtgtg a 51

<210> 1093  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1094 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27843594

<400> 1093  
aggtacagct caggaaggg agcagccct tgctcaggt ctttctggc a 51

<210> 1094  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1093 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27843594

<400> 1094  
aggtacagct caggaaggg agcagccctt gctcaggtc ctttctggca 50

<210> 1095  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1096 is other entry)

<221> misc\_feature



<222> (0)...(0)

<223> Accession number cg27843890

<400> 1095

cgtaggttgac gatctcgccg gtggaggcgt ccttgacgac gatctggcca c

51

<210> 1096

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1095 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27843890

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cgtaggttgac gatctcgccg gtggaagcgt ccttgacgac gatctggcca c

51

<210> 1097

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

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<223> 1 of 2 allelic variants (1098 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27843890

<400> 1097

tggacttcgt cggctctgcgg tacgacgaag ggctcaacat tgccggtggc a

51

<210> 1098

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1097 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27843890

<400> 1098

tggacttcgt cggctctgcgg tacgatgaag ggctcaacat tgccggtggc a

51

<210> 1099  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1100 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27843890  
  
<400> 1099  
acgaagggt caacattgcc ggtggcatcg atgatgagtt tgctcgctg g 51  
  
<210> 1100  
<211> 50  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1099 is other entry)  
  
<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27843890  
  
<400> 1100  
acgaagggt caacattgcc ggtggatcga tgatgagttt gctcgctgg 50  
  
<210> 1101  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1102 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27843890  
  
<400> 1101  
tgagtttgct cgctgggca acacctagca gcaatggcat cgatagtccc t 51  
  
<210> 1102  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1101 is other entry)

<221> misc\_feature  
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<223> Accession number cg27843890

<400> 1102  
tgagtttgct gcgctgggca acaccagca gcaatggcat cgatagtcct t 51

<210> 1103  
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<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1104 is other entry)

<221> misc\_feature  
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<223> Accession number cg27844015

<400> 1103  
ggtaatgcgg aacgcacgtg cctgcgttca gactccattt atcttcaccg t 51

<210> 1104  
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<220>  
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<223> 2 of 2 allelic variants (1103 is other entry)

<221> misc\_feature  
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<223> Accession number cg27844015

<400> 1104  
ggtaatgcgg aacgcacgtg cctgcattca gactccattt atcttcaccg t 51

<210> 1105  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1106 is other entry)

<221> misc\_feature  
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<223> Accession number cg27845127

<400> 1105  
gagcgtgcgc catgatgccg cgactgacac cacctgcggt ccagcccaaa a 51

<210> 1106  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg27845127

<400> 1106  
gagcgtgcgc catgatgccg cgactcacac cacctgcggt ccagcccaaa a 51

<210> 1107  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1108 is other entry)

<221> misc\_feature  
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<223> Accession number cg27845127

<400> 1107  
aaaatcgggt gcttcttcat accaatcacg aggaggtcaa cgttgcccg a 51

<210> 1108  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1107 is other entry)

<221> misc\_feature  
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<223> Accession number cg27845127

<400> 1108  
aaaatcgggt gcttcttcat accaaccacg aggaggtcaa cgttgcccga g 51

<210> 1109  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1110 is other entry)

<221> misc\_feature  
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<223> Accession number cg27845127

<400> 1109  
cataccaatc acgaggaggt caacgctgcc cgagaggtcg actaaggcgt c 51

<210> 1110  
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<210> 1111  
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<223> Accession number cg27845127

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<210> 1112  
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<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1111 is other entry)

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51

<210> 1113

<211> 51

<212> DNA

<213> Homo sapiens

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51

<210> 1114

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agaggtcgac taaggcgctcg acgggtcttc cggacagcac gcgggtctcg a

51

<210> 1115

<211> 47

<212> DNA

<213> Homo sapiens

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47

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47

<210> 1117  
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<400> 1117  
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51

<210> 1118  
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<221> misc\_feature  
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<400> 1118

gttctccgga cagcacgcgg gtctctacct cgacatgggg atgcttatta g

51

<210> 1119

<211> 51

<212> DNA

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gtctcgacct cgacatgggg atgcttatta gcgagcggct tgacgacctc g

51

<210> 1120

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1119 is other entry)

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<223> Accession number cg27845127

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51

<210> 1121

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1122 is other entry)

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51

<210> 1122

<211> 51

<212> DNA

<213> Homo sapiens



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<210> 1123  
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<221> misc\_feature  
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<210> 1124  
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<400> 1124  
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<210> 1125  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 23 and 24

<221> misc\_feature  
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<400> 1125  
ggatcctgtg ccagccgagg aggtccttcc caggctctct caagggtc

48

<210> 1126  
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<220>  
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<223> 2 of 2 allelic variants (1125 is other entry)

<221> misc\_feature  
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<400> 1126  
ggatcctgtg ccagccgagg aggtccttcc ccaggctctc tcaagggtc

49

<210> 1127  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1128 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27845788

<400> 1127  
gcgttttggt aatgagcctg agcagtcatt ctggaccgcc caggctccca g

51

<210> 1128  
<211> 51  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg27845788

<400> 1128

gcgttttgggt aatgagcctg agcagccatg ctggaccgcc caggctccca g

51

<210> 1129

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1130 is other entry)

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<223> Accession number cg27846188

<400> 1129

ttcaaatacca gttcttccac agcaaccagc ccatagttgt tctgtgttct t

51

<210> 1130

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1129 is other entry)

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<223> Accession number cg27846188

<400> 1130

ttcaaatacca gttcttccac agcaatcagc ccatagttgt tctgtgttct t

51

<210> 1131

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1132 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27846188

<400> 1131

ttccacagca accagcccat agttgttctg tgttcttcca cagctgttta c

51

<210> 1132

<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1131 is other entry)

<221> misc\_feature  
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<400> 1132  
ttccacagca accagcccat agttgctctg tgttcttcca cagctgttta c 51

<210> 1133  
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<220>  
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<221> misc\_feature  
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<400> 1133  
tgttcttcca cagctgttta cggtagcctc ctagccactc tcttcagcaa g 51

<210> 1134  
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<220>  
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<221> misc\_feature  
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tgttcttcca cagctgttta cggtaacctc ctagccactc tcttcagcaa g 51

<210> 1135  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 1 of 2 allelic variants (1136 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27846188

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tacctcactt cctccaccgc tcttcagccc ctttgatgtc ccctcagaga a 51

<210> 1136  
<211> 51  
<212> DNA  
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<221> misc\_feature  
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<223> Accession number cg27846188

<400> 1136  
tacctcactt cctccaccgc tcttcgcccc ctttgatgtc ccctcagaga a 51

<210> 1137  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1137  
actagatcca ctgtgctttc cttcaaattc agttctttcca cagcaaccag c 51

<210> 1138  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg27846188

<400> 1138  
actagatcca ctgtgctttc cttcagatcc agttcttcca cagcaaccag c 51

<210> 1139  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg27847752

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gcgcgccctc cctgggtgac aggcgtgact tctttcacaa aaggac 46

<210> 1140  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (21)...(0)  
<223> 2 of 2 allelic variants (1139 is other entry)

<221> misc\_feature  
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<223> Accession number cg27847752

<400> 1140  
gcgcgccctc cctgggtgac ggcgtgact tctttcacaa aaggac 46

<210> 1141  
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<220>  
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<223> 1 of 2 allelic variants (1142 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27847752

<400> 1141  
tgaggccatt cttgcactgc tataaagaaa tacccgagac tgggtaattt a 51

<210> 1142  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1141 is other entry)

<221> misc\_feature  
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<223> Accession number cg27847752

<400> 1142  
tgaggccatt cttgcactgc tataacgaaa taccgagac tgggtaattt a 51

<210> 1143  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg27850121

<400> 1143  
cgtcgccgaa aagccaggcc cggaggtgcc taagtcaggg accgagacgc a 51

<210> 1144  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> Accession number cg27850121

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cgtcgccgaa aagccaggcc cggagtgccct aagtcagggc cagagacgca 50

<210> 1145  
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<220>  
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<223> 1 of 2 allelic variants (1146 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27922967

<400> 1145  
cgcggtgttac caggaaggg gacaggattc ttgcacttt taccctttc t 51

<210> 1146  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1145 is other entry)

<221> misc\_feature  
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<223> Accession number cg27922967

<400> 1146  
cgcggtgttac caggaaggg gacagaattc ttgcacttt taccctttc t 51

<210> 1147  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1148 is other entry)

<221> misc\_feature  
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<223> Accession number cg27926321

<400> 1147  
catcacctcc ctgactgcct ctctaccac ctcccatcac ctccctgact g 51

<210> 1148  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1147 is other entry)



<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27926321

<400> 1148  
catcacctcc ctgactgcct ctctcccccac ctcccatcac ctccctgact g 51

<210> 1149  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1150 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27926378

<400> 1149  
atgggatggt ctgtttttgt ctgtaaagg aaagggatca tttatgttca a 51

<210> 1150  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1149 is other entry)

<221> misc\_feature  
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<223> Accession number cg27926378

<400> 1150  
atgggatggt ctgtttttgt ctgtagagg aaagggatca tttatgttca a 51

<210> 1151  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1152 is other entry)

<221> misc\_feature  
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<223> Accession number cg27926378

<400> 1151  
ttagggaagt aattaagagg ctgtgccctc tgtcacatcc aagtttctgc c 51

<210> 1152  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg27926378

<400> 1152  
ttagggaagt aattaagagg ctgtgcctct gtcacatcca agtttctgcc

50

<210> 1153  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1154 is other entry)

<221> misc\_feature  
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<223> Accession number cg27926378

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agggaagtaa ttaagaggct gtgccctctg tcacatccaa gtttctgcc a

51

<210> 1154  
<211> 50  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1153 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg27926378

<400> 1154  
agggaagtaa ttaagaggct gtgcctctgt cacatccaag tttctgccca 50

<210> 1155  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1156 is other entry)

<221> misc\_feature  
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<223> Accession number cg27926927

<400> 1155  
atcttaagac cctcgatgga tggtgatgcg ggccgcccgg tcggcgaagg g 51

<210> 1156  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1155 is other entry)

<221> misc\_feature  
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<223> Accession number cg27926927

<400> 1156  
atcttaagac cctcgatgga tggtggtgcg ggccgcccgg tcggcgaagg g 51

<210> 1157  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1158 is other entry)

<221> misc\_feature  
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<223> Accession number cg27928117

<400> 1157  
gtggtggagg tcggggcatg ggggtgcccc gccatgttca gattcctgta g 51

<210> 1158  
<211> 50  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1157 is other entry)

<221> misc\_feature

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<400> 1158

gtggtggagg tcggggcatg ggggtgccag ccattgttcag attcctgtag

50

<210> 1159

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1160 is other entry)

<221> misc\_feature

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<223> Accession number cg27928408

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51

<210> 1160

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1159 is other entry)

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51

<210> 1161

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1162 is other entry)

<221> misc\_feature  
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<223> Accession number cg27930889

<400> 1161  
acaattagat gtagtggttag tctgacgatg tgataagaaa acctccccag c 51

<210> 1162  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1161 is other entry)

<221> misc\_feature  
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<223> Accession number cg27930889

<400> 1162  
acaattagat gtagtggttag tctgatgatg tgataagaaa acctccccag c 51

<210> 1163  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1164 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27931448

<400> 1163  
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<210> 1164  
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<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg27931448

<400> 1164  
aaccaccacc ttcggccgcc ccgcgagcca gccagcccg acgcgctcac c 51

<210> 1165  
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<212> DNA  
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<223> 1 of 2 allelic variants (1166 is other entry)

<221> misc\_feature  
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<223> Accession number cg27931448

<400> 1165  
agccagcccg tacgcgtca cccacaggaa cccctcgtc cagtcctca c 51

<210> 1166  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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agccagcccg tacgcgtca cccacgggaa cccctcgtc cagtcctca c 51

<210> 1167  
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<220>  
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<221> misc\_feature  
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<400> 1167  
ccgtacgcgc tcaccacag gaacccctc gtccagtc tcaactaccc t 51

<210> 1168  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1167 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27931448

<400> 1168  
ccgtacgcgc tcacccacag gaacctcctc gtccagtcctc tcaactacccc t 51

<210> 1169  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1170 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27931448

<400> 1169  
gcgctcacc acaggaaccc cctcgtccag tccctcacta cccctcaggg c 51

<210> 1170  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1169 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27931448

<400> 1170  
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<210> 1171  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>

<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27931448

<400> 1171  
acccacagga accccctcgt ccagtccttc actacccttc aggccctgta a

51

<210> 1172  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1171 is other entry)

<221> misc\_feature  
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<223> Accession number cg27931448

<400> 1172  
acccacagga accccctcgt ccagtccttc actacccttc aggccctgta a

51

<210> 1173  
<211> 51  
<212> DNA  
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<221> misc\_feature  
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<223> Accession number cg27931448

<400> 1173  
ccacaggaac cccctcgtcc agtccttcac taccctcag gccctgtcaa g

51

<210> 1174  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1173 is other entry)

<221> misc\_feature  
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<223> Accession number cg27931448

<400> 1174

ccacaggaac cccctcgtec agtccttcac taccctcag gccctgtcaa g

51

<210> 1175

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1176 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27931448

<400> 1175

cgtccagtcc ctactaccc ctgagccct gtcaagccgg cgccggcgca g

51

<210> 1176

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1175 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27931448

<400> 1176

cgtccagtcc ctactaccc ctgagccct gtcaagccgg cgccggcgca g

51

<210> 1177

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1178 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27933823

<400> 1177

cgttaacctc ccacctctgc aatcttgccc gacacctaga tacctgctg c

51

<210> 1178

<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1177 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27933823

<400> 1178  
cgттаacctc ccacctctgc aatctagccc gacacctaga tacctgcgtg c

51

<210> 1179  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1180 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27955069

<400> 1179  
aaaaaaagaa aaaagaaaaa aaaaaagaat gcagtctgtc catttttgtg c

51

<210> 1180  
<211> 50  
<212> DNA  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg27955069

<400> 1180  
aaaaaaagaa aaaagaaaaa aaaaagaatg cagtctgtcc atttttgtgc

50

<210> 1181  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1182 is other entry)

<221> misc\_feature  
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<223> Accession number cg27957329

<400> 1181  
gccgcgggct gagattttcg tctgcccc ctcctgccg ccagcgcct a 51

<210> 1182  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1181 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
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<400> 1182  
gccgcgggct gagattttcg tctgcccc tccctgccg ccagcgcta 50

<210> 1183  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1184 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958374

<400> 1183  
gattggctgt acaggatagc gaatgctgtg gttggagggc acagtcttcc c 51

<210> 1184  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1183 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 1184  
gattggctgt acaggatagc gaatgtgtgg ttggagggca cagtcttccc 50

<210> 1185  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1186 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958800

<400> 1185  
agtggcagga gagaggagat gggggcgtgg cagtgagcga tgaggtcaat c 51

<210> 1186  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1185 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958800

<400> 1186  
agtggcagga gagaggagat ggggggtgtgg cagtgagcga tgaggtcaat c 51

<210> 1187  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 1 of 2 allelic variants (1188 is other entry)

<221> misc\_feature  
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<223> Accession number cg27958800

<400> 1187  
gagatggggg cgtggcagtg agcgatgagg tcaatctgac gaggcctgtg g 51

<210> 1188  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1187 is other entry)

<221> misc\_feature  
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<223> Accession number cg27958800

<400> 1188  
gagatggggg cgtggcagtg agcgacgagg tcaatctgac gaggcctgtg g 51

<210> 1189  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1190 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958800

<400> 1189  
tttggcttca gctaaggag atggccgcca ctgtggagtt ttggggcaga g 51

<210> 1190  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1189 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958800

<400> 1190  
tttggcttca gctaaggag atggcagcca ctgtggagtt ttggggcaga g 51

<210> 1191  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1192 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958800

<400> 1191  
ccgccactgt ggagtttttg ggcagaggga catgctctga cttcccttta a 51

<210> 1192  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1191 is other entry)

<221> misc\_feature  
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<223> Accession number cg27958800

<400> 1192  
ccgccactgt ggagtttttg ggcaggggga catgctctga cttcccttta a 51

<210> 1193  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1194 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958800

<400> 1193  
tctgacttcc ctttaaattg gtcacatgg ctctacgct gagggactac a 51

<210> 1194  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1193 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958800

<400> 1194  
tctgacttcc ctttaaattgg gtcgatgatgg ctctacgct gagggactac a

51

<210> 1195  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1196 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958800

<400> 1195  
catggctcct acgctgaggg actacagggg agaaggggag aaagaccagt t

51

<210> 1196  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27958800

<400> 1196  
catggctcct acgctgaggg actacgggga gaaggggaga aagaccagtt

50

<210> 1197  
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<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1198 is other entry)

<221> misc\_feature  
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<223> Accession number cg27958800

<400> 1197  
cttgagcgcg ccagggacag tggagaccag agtggcagga gagaggagat g 51

<210> 1198  
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<220>  
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<223> 2 of 2 allelic variants (1197 is other entry)

<221> misc\_feature  
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<223> Accession number cg27958800

<400> 1198  
cttgagcgcg ccagggacag tggaggccag agtggcagga gagaggagat g 51

<210> 1199  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1200 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27961578

<400> 1199  
tatggaagag agagagagag agagagtttt tttttcacat ctgaattgat g 51

<210> 1200  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1199 is other entry)



<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg27961578

<400> 1200  
tatggaagag agagagagag agagattttt ttttcacatc tgaattgatg 50

<210> 1201  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1202 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27962034

<400> 1201  
gcccgcccgga ccaagcgtcg gacgcggccc ggcgccgagc catggagcct g 51

<210> 1202  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1201 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg27962034

<400> 1202  
gcccgcccgga ccaagcgtcg gacgcgcccg gcgccgagcc atggagcctg 50

<210> 1203  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)

<223> 1 of 2 allelic variants (1204 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27963505

<400> 1203

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51

<210> 1204

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1203 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg27963505

<400> 1204

cccttcgagg cccggaaga cctccgacc cgctgacaat gctgggcct c

51

<210> 1205

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1206 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg28098037

<400> 1205

gaatggagat aaaagggaat aacaattcaa ctagaaggag aagaagtcct g

51

<210> 1206

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1205 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg28098037

<400> 1206  
gaatggagat aaaaggaat aacaactcaa ctagaaggag aagaagtcct g 51

<210> 1207  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1208 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg28104192

<400> 1207  
taactaccga gagtgggtat ttatctagag agatagaggc ttttggagca g 51

<210> 1208  
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<220>  
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<223> 2 of 2 allelic variants (1207 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg28104192.

<400> 1208  
taactaccga gagtgggtat ttatcaagag agatagaggc ttttggagca g 51

<210> 1209  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1210 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg28117507

<400> 1209  
aggcggaagc tgctccggtg ttgttggtc agtgtgccga tgccggcgtc a 51

<210> 1210  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1209 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg28117507

<400> 1210

aggcgggaagc tgctccggtg ttgtagctc agtgtgccga tgccggcgtc a

51

<210> 1211

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1212 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg28117507

<400> 1211

agtgtgccga tgccggcgtc aagcctttgt tggagggtcc agactggggt t

51

<210> 1212

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1211 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg28117507

<400> 1212

agtgtgccga tgccggcgtc aagcctttgt tggagggtcc agactggggt t

51

<210> 1213

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1214 is other entry)

<221> misc\_feature  
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<400> 1213  
ccggcggtcaa gcctttgttg gaggggtccag actgggggttt attggatcga c

51

<210> 1214  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1213 is other entry)

<221> misc\_feature  
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<223> Accession number cg28117507

<400> 1214  
ccggcggtcaa gcctttgttg gaggggtccag actgggggttt attggatcga c

51

<210> 1215  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1216 is other entry)

<221> misc\_feature  
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<223> Accession number cg28350841

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gggacttgga caggcacggg ccctggcatg gcggggccagg tccacctcgg c

51

<210> 1216  
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<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
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<221> misc\_feature  
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<221> misc\_feature

<222> (0)...(0)  
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<400> 1216  
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<210> 1217  
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<400> 1217  
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<210> 1218  
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<221> misc\_feature  
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<223> Accession number cg28375854

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gcggggggccc agccatcttg cacttgatgg atggcacacg aggccagctg c 51

<210> 1219  
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<223> Accession number cg28376296

<400> 1219  
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<210> 1220  
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50

<210> 1221  
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<221> misc\_feature  
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<400> 1221  
agatagatag atagatagat agatgataga tagatagata gatagataga t

51

<210> 1222  
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agatagatag atagatagat agatgtagat agatagatag atagatagat

50

<210> 1223

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1224 is other entry)

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<223> Accession number cg28388611

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51

<210> 1224

<211> 50

<212> DNA

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<223> Accession number cg28388611

<400> 1224

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<210> 1225

<211> 51

<212> DNA

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<223> Accession number cg28389525

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51



<210> 1226

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1225 is other entry)

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<223> Accession number cg28389525

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51

<210> 1227

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1228 is other entry)

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<223> Accession number cg28389525

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<210> 1228

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<223> Accession number cg28389525

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<210> 1229

<211> 51

<212> DNA

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<210> 1230  
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<400> 1230  
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<210> 1231  
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<210> 1232  
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51

<210> 1233

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<223> 1 of 2 allelic variants (1234 is other entry)

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<223> Accession number cg28389807

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51

<210> 1234

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1233 is other entry)

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<223> Accession number cg28389807

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51

<210> 1235

<211> 51

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<223> 1 of 2 allelic variants (1236 is other entry)

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51

<210> 1236

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<223> 1 of 2 allelic variants (1238 is other entry)

<221> misc\_feature  
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<210> 1238  
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<210> 1239  
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<223> 1 of 2 allelic variants (1240 is other entry)

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<223> Accession number cg28397512

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51

<210> 1240

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<223> Accession number cg28397512

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gcctccacct gtgctagggtg ggccctctgg gttctaaggc atctctgtat

50

<210> 1241

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1242 is other entry)

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<223> Accession number cg28399769

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51

<210> 1242

<211> 50

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<213> Homo sapiens

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<210> 1243  
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gagtggttca ccttttactt ggtcaatcag ggggtttgtg ttcccaggaa c 51

<210> 1244  
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<210> 1245  
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<210> 1246  
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<210> 1247  
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<221> misc\_feature  
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<210> 1248  
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<400> 1248  
tgtccacgaa atacacccca aacccaaagc cttctctcca ccaagtccaa g 51

<210> 1249  
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<400> 1249  
gtggatggca gccagagaga ctgctgaggt tctggatggt agggccttga t 51

<210> 1250  
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gtggatggca gccagagaga ctgctcaggt tctggatggt agggccttga t 51

<210> 1251  
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<210> 1252  
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<212> DNA  
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<220>  
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<210> 1253  
<211> 51  
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51

<210> 1254  
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<400> 1254  
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51

<210> 1255  
<211> 51  
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<222> (0)...(0)

<223> Accession number cg28473092

<400> 1255

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51

<210> 1256

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1255 is other entry)

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<223> Accession number cg28473092

<400> 1256

gacgggtaag gatttgcgag ctaatgacga tcggagcgtc accctcgagc a

51

<210> 1257

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1258 is other entry)

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ggatttgcga gctaataacg atcggagcgt caccctcgag catcgtcacc t

51

<210> 1258

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1257 is other entry)

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<210> 1259  
<211> 51  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<400> 1259  
gcgagctaataacgacgcgtcaccctcgagcatcgtcacctcgatgc 51

<210> 1260  
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<221> misc\_feature  
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<400> 1260  
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<210> 1261  
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<221> misc\_feature  
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<210> 1262  
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<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1261 is other entry)

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51

<210> 1263

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1264 is other entry)

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<400> 1263

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51

<210> 1264

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1263 is other entry)

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51

<210> 1265

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1266 is other entry)

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<400> 1265  
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<210> 1266  
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gtttatacga ctggatctcg ttgatgctga gcaggagtgg ttcgatcatcc a 51

<210> 1267  
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<220>  
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<210> 1268  
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47

<210> 1269

<211> 51

<212> DNA

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<223> Accession number cg28785423

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51

<210> 1270

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1269 is other entry)

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<223> Accession number cg28785423

<400> 1270

gggttttagct agcatgtagc aagcccttaa tgactgcagc tattatcata a

51

<210> 1271

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1272 is other entry)

<221> misc\_feature

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<223> Accession number cg28785423

<400> 1271

atgtagcaag cccttaatga ctgcagctat tatkataatt agctctgtat g

51

<210> 1272

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1271 is other entry)

<221> misc\_feature  
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<400> 1272  
atgtagcaag cccttaatga ctgcaactat tatcataatt agctctgtat g 51

<210> 1273  
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<223> 1 of 2 allelic variants (1274 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg28785423

<400> 1273  
ctattatcat aattagctct gtatgacttt ttacattcat cagatccctt a 51

<210> 1274  
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<212> DNA  
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<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg28785423

<400> 1274  
ctattatcat aattagctct gtatgctttt tacattcatc agatccctta 50

<210> 1275  
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<212> DNA  
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<220>

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<221> misc\_feature  
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<223> Accession number cg28786600

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ggatgcaccc acgctgggcg cccagcggcc tetaaccgcc gccccagccc a

51

<210> 1276  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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50

<210> 1277  
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<221> misc\_feature  
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51

<210> 1278  
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<223> 2 of 2 allelic variants (1277 is other entry)

<221> misc\_feature

<222> (25)...(26)

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<223> Accession number cg28790405

<400> 1278

ggatatgctc actaccggg gcgtaccgac gcgacttcga ggaaaacgtg

50

<210> 1279

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1280 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg28814812

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taataacagc agagttaccc taagacatac aatctgctgc gtgtatgcta a

51

<210> 1280

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1279 is other entry)

<221> misc\_feature

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<223> Accession number cg28814812

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51

<210> 1281

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1282 is other entry)

<221> misc\_feature  
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<223> Accession number cg28821175

<400> 1281  
actattgccca atatttttaaa acactaattt gccttttaaac tagagattta a 51

<210> 1282  
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<220>  
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<223> 2 of 2 allelic variants (1281 is other entry)

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<223> Accession number cg28821175

<400> 1282  
actattgccca atatttttaaa acacttattt gccttttaaac tagagattta a 51

<210> 1283  
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<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1284 is other entry)

<221> misc\_feature  
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<223> Accession number cg28955364

<400> 1283  
caataaccgc ggtgggtgtg cagcaggaag tttccagta cctgatagcc g 51

<210> 1284  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1283 is other entry)

<221> misc\_feature  
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<400> 1284  
caataaccgc ggtgggtgtg cagcaagaag tttccagta cctgatagcc g 51

<210> 1285  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1285  
tgtgcagcag gaagttttcc agtacctgat agccgtcacc ttcgggtgcg t

51

<210> 1286  
<211> 51  
<212> DNA  
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1285 is other entry)

<221> misc\_feature  
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tgtgcagcag gaagttttcc agtacttgat agccgtcacc ttcgggtgcg t

51

<210> 1287  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1287  
agccgtcacc ttcgggtgcg ttgatctcgt aatggaatcg agcgtgtca c

51

<210> 1288  
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<400> 1288  
agccgtcacc ttcgggtgcg ttgatgtcgt aatggaatcg agcgctgtca c 51

<210> 1289  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg28955364

<400> 1289  
cagttttgaa tcgcatggc cttggctacg ggggtagatt tccccttgat a 51

<210> 1290  
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<220>  
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<400> 1290  
cagttttgaa tcgcatggc cttgggtacg ggggtagatt tccccttgat a 51

<210> 1291  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1292 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg28955364

<400> 1291  
tccccttgat aattcgggta gttactccc ctatgtcgga tggaacgttg g 51

<210> 1292  
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<221> misc\_feature  
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<223> Accession number cg28955364

<400> 1292  
tccccttgat aattcgggta gttactccc ctatgtcgga tggaacgttg g 51

<210> 1293  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1294 is other entry)

<221> misc\_feature  
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<223> Accession number cg28955364

<400> 1293  
ttgataattc ggtaggttaa ctcccctatg tcggatggaa cgttggcagg g 51

<210> 1294  
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<220>  
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<223> 2 of 2 allelic variants (1293 is other entry)

<221> misc\_feature  
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<400> 1294  
ttgataattc ggtaggttaa ctcccctatg tcggatggaa cgttggcagg g 51

<210> 1295  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1296 is other entry)

<221> misc\_feature  
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<223> Accession number cg28955364

<400> 1295  
aattcgggta gttactccc ctatgtcggg tggaacggtg gcagggactt c

51

<210> 1296  
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<220>  
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<223> 2 of 2 allelic variants (1295 is other entry)

<221> misc\_feature  
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<223> Accession number cg28955364

<400> 1296  
aattcgggta gttactccc ctatgccgga tggaacggtg gcagggactt c

51

<210> 1297  
<211> 51  
<212> DNA  
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<223> 1 of 2 allelic variants (1298 is other entry)

<221> misc\_feature  
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<223> Accession number cg28955364

<400> 1297  
actcccctat gtcggatgga acgttggcag ggacttcggt gtacaccgag t

51

<210> 1298  
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<212> DNA  
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<221> misc\_feature  
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<400> 1298  
actcccctat gtcggatgga acgtagcag ggacttcggt gtacaccgag t 51

<210> 1299  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1300 is other entry)

<221> misc\_feature  
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<400> 1299  
gggacttcgg tgtacaccga gttatgtggg gtgccggctt tcgcgttattc g 51

<210> 1300  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg28955364

<400> 1300  
gggacttcgg tgtacaccga gttatttggg gtgccggctt tcgcgttattc g 51

<210> 1301  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1302 is other entry)

<221> misc\_feature  
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<223> Accession number cg28955364

<400> 1301

acaccgagtt atgtgggggtg cgggctttcg cgttatcgaa ggttactgga t

51

<210> 1302

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1301 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg28955364

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acaccgagtt atgtgggggtg cgggccttcg cgttatcgaa ggttactgga t

51

<210> 1303

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1304 is other entry)

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<223> Accession number cg28955364

<400> 1303

acggaatacc ttcaagtcgt gccatgagtg ccattgacgc cgcgaaatgg a

51

<210> 1304

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1303 is other entry)

<221> misc\_feature

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<223> Accession number cg28955364

<400> 1304

acggaatacc ttcaagtcgt gccataagtg ccattgacgc cgcgaaatgg a

51

<210> 1305



<211> 51  
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<220>  
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<223> 1 of 2 allelic variants (1306 is other entry)

<221> misc\_feature  
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<400> 1305  
acgccgcgaa atggatgcaa taaccgcggt ggggtgtgcag caggaagttt t 51

<210> 1306  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (1305 is other entry)

<221> misc\_feature  
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<400> 1306  
acgccgcgaa atggatgcaa taaccacggt ggggtgtgcag caggaagttt t 51

<210> 1307  
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<220>  
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<223> 1 of 2 allelic variants (1308 is other entry)

<221> misc\_feature  
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<223> Accession number cg28955364

<400> 1307  
atggatgcaa taaccgcggt ggggtgtgcag caggaagttt tccagtacct g 51

<210> 1308  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1307 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 1308  
atggatgcaa taaccgcggt ggggtgcgag caggaagttt tccagtacct g 51

<210> 1309  
<211> 51  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1310 is other entry)

<221> misc\_feature  
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<223> Accession number cg28961882

<400> 1309  
aacagaatgc aaacaatcaa aaacatagtc catttaaact atctgggcga c 51

<210> 1310  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg28961882

<400> 1310  
aacagaatgc aaacaatcaa aaacaagtcc atttaaacta tctgggcgac 50

<210> 1311  
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<212> DNA  
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<221> misc\_feature  
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<221> misc\_feature  
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<400> 1311  
tggcagttct gctgagattt tttttaggac tttcctgaag cttagcttca

50

<210> 1312  
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<220>  
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<223> 2 of 2 allelic variants (1311 is other entry)

<221> misc\_feature  
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<400> 1312  
tggcagttct gctgagattt tttttagga cttcctgaa gcttagcttc a

51

<210> 1313  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1314 is other entry)

<221> misc\_feature  
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<400> 1313  
acatagtcca tttaaactat ctgggcgaca aaatgggcac ttaattttac t

51

<210> 1314  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1313 is other entry)

<221> misc\_feature

<222> (0)...(0)  
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<400> 1314  
acatagtcca tttaaactat ctgggtgaca aaatgggcac ttaattttac t 51

<210> 1315  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1316 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg28970326

<400> 1315  
catggcctgt catggcgtag tcttcacgt cgtaaagtat gagacaatcc a 51

<210> 1316  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1315 is other entry)

<221> misc\_feature  
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<223> Accession number cg28970326

<400> 1316  
catggcctgt catggcgtag tcttctacgt cgtaaagtat gagacaatcc a 51

<210> 1317  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1318 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 1317  
gggtccatga ggagttcgtc caaggttcga actcattacc gtcgaatacg

50

<210> 1318  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1317 is other entry)

<221> misc\_feature  
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<223> Accession number cg28970326

<400> 1318  
gggtccatga ggagttcgtc caagggttcg aactcattac cgtcgaatac g

51

<210> 1319  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1320 is other entry)

<221> misc\_feature  
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<223> Accession number cg28972181

<400> 1319  
agctggttct ctccgaaatg catttggtg cagcgtcggg tcattacgtc c

51

<210> 1320  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1319 is other entry)

<221> misc\_feature  
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51

<210> 1321  
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<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1322 is other entry)

<221> misc\_feature  
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<400> 1321  
aaatgcattt ggggtgcagcg tcgggtcatt acgtcccggg ggtagagcta c 51

<210> 1322  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1321 is other entry)

<221> misc\_feature  
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<223> Accession number cg28972181

<400> 1322  
aaatgcattt ggggtgcagcg tcggggcatt acgtcccggg ggtagagcta c 51

<210> 1323  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg28972181

<400> 1323  
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<210> 1324  
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<223> Accession number cg28972181

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51

<210> 1325

<211> 51

<212> DNA

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<223> Accession number cg28986449

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51

<210> 1326

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg28986449

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51

<210> 1327

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1328 is other entry)

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<223> Accession number cg29004129

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cgcaagattt cgaggcaact cggtatcact cactgtgctt gaccacgttg g 51

<210> 1328  
<211> 51  
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<213> Homo sapiens

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<221> misc\_feature  
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<223> Accession number cg29004129

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cgcaagattt cgaggcaact cggtaccact cactgtgctt gaccacgttg g 51

<210> 1329  
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<223> Accession number cg29012565

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cccattcgga aaatcaatcc gggggcgctg gctgggtag tcacggcggg c 51

<210> 1330  
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<221> misc\_feature  
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<210> 1331  
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<221> misc\_feature  
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<223> Accession number cg29012565

<400> 1331  
ggcaaagcca cggttgtccc tcctgaatga gctagattac cctaccctac c 51

<210> 1332  
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<221> misc\_feature  
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<400> 1332  
ggcaaagcca cggttgtccc tcctggatga gctagattac cctaccctac c 51

<210> 1333  
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atagggggga tattttgggg tggtagtagt ggtggtctgt tttccagata t 51

<210> 1334  
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<221> misc\_feature  
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<400> 1334  
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<210> 1335  
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<213> Homo sapiens

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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29141731

<400> 1335  
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<210> 1336  
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<221> misc\_feature  
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<223> Accession number cg29141731

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<210> 1337  
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<213> Homo sapiens

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<221> misc\_feature  
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<223> Accession number cg29144273

<400> 1337

atgggataag atgtaagttt ttaatactag caatgtacac tactcttttt t 51

<210> 1338  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1337 is other entry)

<221> misc\_feature  
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<223> Accession number cg29144273

<400> 1338  
atgggataag atgtaagttt ttaatgctag caatgtacac tactcttttt t 51

<210> 1339  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29144339

<400> 1339  
aagcaaaacc catcgggggg gggggacatc tacatgccat ctttggtgct 50

<210> 1340  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg29144339

<400> 1340  
aagcaaaacc catcgggggg ggggggacat ctacatgcca tctttggtgc t 51

<210> 1341  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg29195033

<400> 1341  
ccgctcatag tgctgctcagt cagaatcttc atcattgccg atacgtgata g

51

<210> 1342  
<211> 51  
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<221> misc\_feature  
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<223> 2 of 2 allelic variants (1341 is other entry)

<221> misc\_feature  
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<223> Accession number cg29195033

<400> 1342  
ccgctcatag tgctgctcagt cagaaccttc atcattgccg atacgtgata g

51

<210> 1343  
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<223> 1 of 2 allelic variants (1344 is other entry)

<221> misc\_feature  
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<400> 1343  
ccgccacccc actctaggcc tcctgtggt tcagcatcct caaccccgct t

51

<210> 1344  
<211> 51  
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<220>

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<221> misc\_feature  
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<223> Accession number cg29202844

<400> 1344  
ccgccacccc actctaggcc tccctatggt tcagcatcct caaccccgct t 51

<210> 1345  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1346 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29207528

<400> 1345  
cgggtcaggg gcgttcgcgg cgccagctgg cacaacttcg cgaccggcga c 51

<210> 1346  
<211> 50  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg29207528

<400> 1346  
cgggtcaggg gcgttcgcgg cgccactggc acaacttcgc gaccggcgac 50

<210> 1347  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1348 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29207528

<400> 1347

cttcgacgcc aacgagcttg ccgtagctcc tgatactgac accgtcatcc a

51

<210> 1348

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1347 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29207528

<400> 1348

cttcgacgcc aacgagcttg ccgtaactcc tgatactgac accgtcatcc a

51

<210> 1349

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1350 is other entry)

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<223> Accession number cg29207528

<400> 1349

tactgacacc gtcacccagg gagtcgggcc cggcctagcc ctctcgatc c

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<210> 1350

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<223> 2 of 2 allelic variants (1349 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 1350  
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<210> 1351  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg29207528

<400> 1351  
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51

<210> 1352  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1351 is other entry)

<221> misc\_feature  
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<223> Accession number cg29207528

<400> 1352  
cctcgctcgac acatgccgat aaccaacag cccaggcatg gcgcgatttc g

51

<210> 1353  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1354 is other entry)

<221> misc\_feature  
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<223> Accession number cg29207528

<400> 1353  
ctgcgcgtcg cagatgccgc acaggcacgg gtcaggggcg ttcgcggcgc c

51

<210> 1354  
<211> 50  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 1354  
ctgcgcgtcg cagatgccgc acaggacggg tcaggggcgt tcgcggcgcc

50

<210> 1355  
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<220>  
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<222> (26)...(0)  
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<221> misc\_feature  
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<223> Accession number cg29210581

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51

<210> 1356  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1356  
tttttcctga gttatggaag gaatgataat tggggaattc aggcttaaaa t

51

<210> 1357



<211> 51  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1358 is other entry)

<221> misc\_feature  
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<223> Accession number cg29216983

<400> 1357  
gcattctgtg aggctaccgc aggctctggc gtaaagcagt ggagccaggt c 51

<210> 1358  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1357 is other entry)

<221> misc\_feature  
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<223> Accession number cg29216983

<400> 1358  
gcattctgtg aggctaccgc aggctttggc gtaaagcagt ggagccaggt c 51

<210> 1359  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1360 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29217243

<400> 1359  
ggcgcggcgc tccatccaaa tcgatctggg catccgcccc tgtcacgcga a 51

<210> 1360  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 2 of 2 allelic variants (1359 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29217243

<400> 1360  
ggcgcggcgc tccatccaaa tcgatttggg catccgcccc tgtcaccgca a 51

<210> 1361  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1362 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29217243

<400> 1361  
cagcaccatt accgacgagc cgagcaccgt ccagataggc cggcgatcc c 51

<210> 1362  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1361 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29217243

<400> 1362  
cagcaccatt accgacgagc cgagcgccgt ccagataggc cggcgatcc c 51

<210> 1363  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1364 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29217243

<400> 1363  
gccgagcacc gtccagatag gcccggcgat cccatgtcc gcagccactg a 51

<210> 1364  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1363 is other entry)

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<222> (0)...(0)  
<223> Accession number cg29217243

<400> 1364  
gccgagcacc gtccagatag gcccgacgat cccatgtcc gcagccactg a 51

<210> 1365  
<211> 51  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1366 is other entry)

<221> misc\_feature  
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<400> 1365  
ttcctagatc cgccaaccg cgacggccag cgtcctcaat gagggttctc g 51

<210> 1366  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1365 is other entry)

<221> misc\_feature  
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<223> Accession number cg29217243

<400> 1366  
ttcctagatc cgccaaccg cgacgtccag cgtcctcaat gagggttctc g 51

<210> 1367  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1368 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29217243

<400> 1367  
cgcgacggcc agcgctcctca atgaggggttc tcggcccggc tgtctctact a 51

<210> 1368  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1367 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29217243

<400> 1368  
cgcgacggcc agcgctcctca atgagaggttc tcggcccggc tgtctctact a 51

<210> 1369  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1370 is other entry)

<221> misc\_feature  
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<223> Accession number cg29234950

<400> 1369  
caaccacagg gcccctctcc gaggggtaccc cacaggccac acggtggcga c 51

<210> 1370  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1369 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29234950

<400> 1370

caaccagggg gcccctctcc gagggcaccc cacaggccac acggtggcga c

51

<210> 1371

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1372 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29237731

<400> 1371

ctcaatcctg acagataccg atcataaggc aatggcactc caggagtatt t

51

<210> 1372

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29237731

<400> 1372

ctcaatcctg acagataccg atcatgaggc aatggcactc caggagtatt t

51

<210> 1373

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1374 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29237731

<400> 1373  
aatcctgaca gataccgatc ataaggcaat ggcactccag gagtatttcc t 51

<210> 1374  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1373 is other entry)

<221> misc\_feature  
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<223> Accession number cg29237731

<400> 1374  
aatcctgaca gataccgatc ataagccaat ggcactccag gagtatttcc t 51

<210> 1375  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1376 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29239003

<400> 1375  
ggattccact ttccctgtcc cctacctccc caaactcttg caagaaaata a 51

<210> 1376  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1375 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29239003

<400> 1376  
ggattccact ttccctgtcc cctacttccc caaactcttg caagaaaata a 51

<210> 1377  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1378 is other entry)

<221> misc\_feature

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<400> 1377

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51

<210> 1378

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<223> Accession number cg29250853

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51

<210> 1379

<211> 51

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<223> 1 of 2 allelic variants (1380 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29255997

<400> 1379

aaacaaggaa gagtaggatg gaatcggaat aaaacagtga aagaacatta t

51

<210> 1380

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1379 is other entry)

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<210> 1381  
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<223> Accession number cg29255997

<400> 1381  
aggatggaat cggaataaaa cagtgaaga acattattct ttgtaccgtg a 51

<210> 1382  
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (1381 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29255997

<400> 1382  
aggatggaat cggaataaaa cagtgaaga acattattct ttgtaccgtg a 51

<210> 1383  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1384 is other entry)

<221> misc\_feature



<222> (0)...(0)  
<223> Accession number cg29256466

<400> 1383  
tgaatataag gctagataat ggagcgtttg tgatcccttg tctattctca g 51

<210> 1384  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> Accession number cg29256466

<400> 1384  
tgaatataag gctagataat ggagcatttg tgatcccttg tctattctca g 51

<210> 1385  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1386 is other entry)

<221> misc\_feature  
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<223> Accession number cg29260975

<400> 1385  
ctgcaatgag ctgtgaccac gccactgcac tccagcctgg gcgacagagc a 51

<210> 1386  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1385 is other entry)

<221> misc\_feature  
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<223> Accession number cg29260975

<400> 1386  
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<210> 1387

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1388 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29260975

<400> 1387

ccagcctggg cgacagagca agaccatgat atttcaagaa aagtccttga g

51

<210> 1388

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1387 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29260975

<400> 1388

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51

<210> 1389

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1390 is other entry)

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51

<210> 1390

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1389 is other entry)

<221> misc\_feature  
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<223> Accession number cg29264501

<400> 1390  
ctccccaacc cactccccag taacacaggg ttttccccga ttctcacagt g 51

<210> 1391  
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<223> 1 of 2 allelic variants (1392 is other entry)

<221> misc\_feature  
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<223> Accession number cg29337682

<400> 1391  
gtggtgcatg cctgtaatcc cagcactttg ggaggctgag gcaggaggat c 51

<210> 1392  
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<220>  
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<223> 2 of 2 allelic variants (1391 is other entry)

<221> misc\_feature  
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<223> Accession number cg29337682

<400> 1392  
gtggtgcatg cctgtaatcc cagcaatttg ggaggctgag gcaggaggat c 51

<210> 1393  
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<220>  
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<223> 1 of 2 allelic variants (1394 is other entry)

<221> misc\_feature  
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<223> Accession number cg29345077

<400> 1393

actcccgacc tcaggtgatc cgcccacctc ggccctcccaa agtgctggga t

51

<210> 1394

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg29345077

<400> 1394

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51

<210> 1395

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1396 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29345273

<400> 1395

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51

<210> 1396

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1395 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29345273

<400> 1396

cttatggcac gggggctgca gcttgccctc ctctccagg tgggatgcct c

51

<210> 1397

<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1398 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29345769

<400> 1397  
ctgtattaag acttaaaactc ctgccgcacc tggagtaata aacttgtggg a 51

<210> 1398  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1397 is other entry)

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<222> (0)...(0)  
<223> Accession number cg29345769

<400> 1398  
ctgtattaag acttaaaactc ctgccacacc tggagtaata aacttgtggg a 51

<210> 1399  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1400 is other entry)

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<223> Accession number cg29346973

<400> 1399  
agttatctca taattaaaaa aaaaaactag ctcgtagaa ttagaatcta a 51

<210> 1400  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 2 of 2 allelic variants (1399 is other entry)

<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29346973

<400> 1400  
agttatctca taattaaaaa aaaaactagc tcgttagaat tagaatctaa 50

<210> 1401  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1402 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29348101

<400> 1401  
ccgctcaggc tgctgctgcg ggcgcctgtgt ggtactccgc cgaaggcgat a 51

<210> 1402  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1401 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29348101

<400> 1402  
ccgctcaggc tgctgctgcg ggcgctgtgt ggtactccgc cgaaggcgat a 51

<210> 1403  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1404 is other entry)

<221> misc\_feature  
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<400> 1403  
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<210> 1404  
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<223> 2 of 2 allelic variants (1403 is other entry)

<221> misc\_feature  
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<400> 1404  
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<210> 1405  
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<223> 1 of 2 allelic variants (1406 is other entry)

<221> misc\_feature  
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<400> 1405  
ataagtggaa ggtcgatacc aacggtgaca agagcaaagt tgttgccgat t 51

<210> 1406  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1405 is other entry)

<221> misc\_feature  
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<400> 1406

ataagtggaa ggtcgatacc aacggcgaca agagcaaagt tgttgccgat t

51

<210> 1407

<211> 44

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1408 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29348101

<400> 1407

cgacgacaag agcgctgtca ctgacccccg ttggagcgac gcgt

44

<210> 1408

<211> 44

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1407 is other entry)

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<222> (0)...(0)

<223> Accession number cg29348101

<400> 1408

cgacgacaag agcgctgtca ctgacgccccg ttggagcgac gcgt

44

<210> 1409

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1410 is other entry)

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<223> Accession number cg29348101

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51

<210> 1410

<211> 51

<212> DNA

<213> Homo sapiens



<220>  
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<223> 2 of 2 allelic variants (1409 is other entry)

<221> misc\_feature  
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<223> Accession number cg29348101

<400> 1410  
tgctttcctc cgccaagaag gctgctgccca agggcaagta catcctcgga t 51

<210> 1411  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1412 is other entry)

<221> misc\_feature  
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<223> Accession number cg29348101

<400> 1411  
tttctctccgc caagaaggct gccgccaagg gcaagtacat cctcggattt g 51

<210> 1412  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1411 is other entry)

<221> misc\_feature  
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<400> 1412  
tttctctccgc caagaaggct gccgctaagg gcaagtacat cctcggattt g 51

<210> 1413  
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<223> 1 of 2 allelic variants (1414 is other entry)

<221> misc\_feature  
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<223> Accession number cg29348230

<400> 1413  
tcagaggggtg agaaagccca gagcatttta catgttttagg attttgactt t

51

<210> 1414  
<211> 50  
<212> DNA  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 1414  
tcagaggggtg agaaagccca gagcatttac atgttttagga ttttgacttt

50

<210> 1415  
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<223> 1 of 2 allelic variants (1416 is other entry)

<221> misc\_feature  
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51

<210> 1416  
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<223> 2 of 2 allelic variants (1415 is other entry)

<221> misc\_feature  
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<223> Accession number cg29348328

<400> 1416

tgcattacca agagctgacg atctccggag gatcgaatgc cagtcgggca g

51

<210> 1417

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1418 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29348328

<400> 1417

tctctggagg atcgaatgcc agtcgggcag acgttcaccg ggcggtcgac a

51

<210> 1418

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1417 is other entry)

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<223> Accession number cg29348328

<400> 1418

tctctggagg atcgaatgcc agtcgagcag acgttcaccg ggcggtcgac a

51

<210> 1419

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1420 is other entry)

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atgctcggac ggggaaatat cgacgggacc cccattgtca ctcacacttt t

51

<210> 1420

<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (1419 is other entry)

<221> misc\_feature  
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<400> 1420  
atgctcggac ggggaaatat cgacgagacc cccattgtca ctcacacttt t 51

<210> 1421  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1422 is other entry)

<221> misc\_feature  
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<223> Accession number cg29348328

<400> 1421  
tgctcggacg gggaaatatc gacgggaccc ccattgtcac tcacactttt g 51

<210> 1422  
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<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1421 is other entry)

<221> misc\_feature  
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<223> Accession number cg29348328

<400> 1422  
tgctcggacg gggaaatatc gacggaaccc ccattgtcac tcacactttt g 51

<210> 1423  
<211> 51  
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<220>  
<221> misc\_feature

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<223> 1 of 2 allelic variants (1424 is other entry)

<221> misc\_feature  
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<223> Accession number cg29348328

<400> 1423  
cttttggcct gtcccagtg accgaggctg ttgacgccgt gcgcggtcac g 51

<210> 1424  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1423 is other entry)

<221> misc\_feature  
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<223> Accession number cg29348328

<400> 1424  
cttttggcct gtcccagtg accgaagctg ttgacgccgt gcgcggtcac g 51

<210> 1425  
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<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1426 is other entry)

<221> misc\_feature  
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<223> Accession number cg29348328

<400> 1425  
gctgttgacg ccgtgcgcgg tcacgccggc gtcaagatcg ctatcgatcc c 51

<210> 1426  
<211> 51  
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<220>  
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<221> misc\_feature  
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gctgttgacg ccgtgcgcgg tcacgtcggc gtcaagatcg ctatcgatcc c 51

<210> 1427  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1428 is other entry)

<221> misc\_feature  
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<400> 1427  
ttgacgcgct gcgcggtcac gccggcgtca agatcgctat cgatccccgc c 51

<210> 1428  
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<221> misc\_feature  
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<400> 1428  
ttgacgcgct gcgcggtcac gccgggtgca agatcgctat cgatccccgc c 51

<210> 1429  
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<220>  
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<223> 1 of 2 allelic variants (1430 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29348328

<400> 1429  
gacgcgtgag ttggtttgct gggtttccca agggatcaac gacgaccatc a 51

<210> 1430  
<211> 51

<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1429 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29348328

<400> 1430  
gacgcgtgag ttggtttgct ggtttcccca agggatcaac gacgaccatc a

51

<210> 1431  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2, allelic variants (1432 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29348397

<400> 1431  
ttatgttatt tataaaacga ccaaggaaat gaatgtaatt tggctttcat a

51

<210> 1432  
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51

<210> 1433  
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<223> 1 of 2 allelic variants (1434 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29348993

<400> 1433

gtttgtttgt ttttaactttt tttttttcat tctcgctgta gatagcctga a

51

<210> 1434

<211> 50

<212> DNA

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<223> Accession number cg29348993

<400> 1434

gtttgtttgt ttttaactttt ttttttcatt ctcgctgtag atagcctgaa

50

<210> 1435

<211> 51

<212> DNA

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<223> Accession number cg29348993

<400> 1435

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<210> 1437  
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<210> 1438  
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<400> 1438  
tcgctgtaga tagcctgaat ccaaaaaaaaa ccaaaggagg ttatccaagt a 51

<210> 1439  
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<223> Accession number cg29349829

<400> 1439

cataggcacc gcgtgaaggg caccgtaaga atcttcccga atgctcctgt c

51

<210> 1440

<211> 50

<212> DNA

<213> Homo sapiens

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<223> Accession number cg29349829

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<210> 1441

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<223> Accession number cg29349990

<400> 1441

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<210> 1442

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1441 is other entry)

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<223> Accession number cg29349990

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<210> 1443  
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<210> 1444  
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<400> 1444  
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<210> 1445  
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<223> 1 of 2 allelic variants (1446 is other entry)

<221> misc\_feature  
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<223> Accession number cg29352964

<400> 1445  
ggaaggtgtg cggatactta ttgtcgggtgc ggcacgtcc atccacaccg t 51

<210> 1446  
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (1445 is other entry)

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<223> Accession number cg29352964

<400> 1446

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<210> 1447

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1448 is other entry)

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gccgtcactc cattgatccc cgagtcgga tccatctggc cccacacggc g

51

<210> 1448

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1447 is other entry)

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<223> Accession number cg29352964

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<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (1450 is other entry)

<221> misc\_feature  
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<223> Accession number cg29352964

<400> 1449  
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<210> 1450  
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<210> 1451  
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<400> 1451  
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<210> 1452  
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51

<210> 1453

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1454 is other entry)

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<223> Accession number cg29352964

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51

<210> 1454

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1453 is other entry)

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<223> Accession number cg29352964

<400> 1454

ccccgacgct gctgtcgggtg tggggaagtg acgtttacga ttccccccgg g

51

<210> 1455

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1456 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29354835

<400> 1455

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51

<210> 1456

<211> 51

<212> DNA

<213> Homo sapiens

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<223> Accession number cg29354835

<400> 1456  
ggggcctttc ctgtgtgaca cttcctgtga gggctctcaga ccccttgag a 51

<210> 1457  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1458 is other entry)

<221> misc\_feature  
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<223> Accession number cg29357657

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<210> 1458  
<211> 50  
<212> DNA  
<213> Homo sapiens

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<223> Accession number cg29357657

<400> 1458  
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<210> 1459  
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<400> 1459  
ttgctatcgc tcgcgctttc gcctctgaac ccaaaatatt gtttgcggat g 51

<210> 1460  
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ttgctatcgc tcgcgctttc gcctcgaacc caaaatattg tttgcggatg 50

<210> 1461  
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<221> misc\_feature  
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<223> Accession number cg29360589

<400> 1461  
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<210> 1462  
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<223> 2 of 2 allelic variants (1461 is other entry)

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<222> (0)...(0)

<223> Accession number cg29360589

<400> 1462

gcccgtgtg acaccattgg tactcgggtc cgtctgacct tcgacccaga a

51

<210> 1463

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1464 is other entry)

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<223> Accession number cg29360589

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51

<210> 1464

<211> 50

<212> DNA

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<223> Nucleotide deleted between bases 25 and 26

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<222> (0)...(0)

<223> Accession number cg29360589

<400> 1464

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<210> 1465

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<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1466 is other entry)

<221> misc\_feature  
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<223> Accession number cg29363109

<400> 1465  
taatccagtg ctcccggtg taccaccctg cctattcaca gtgggcacac t 51

<210> 1466  
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<210> 1467  
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<400> 1467  
aggagctgtc cagggttctg gagacgaaac ggagcccgct gggaactgtc c 51

<210> 1468  
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<220>  
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<223> 2 of 2 allelic variants (1467 is other entry)

<221> misc\_feature  
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<223> Accession number cg29495773

<400> 1468  
aggagctgtc cagggttctg gagactaaac ggagcccgct gggaactgtc c 51

<210> 1469  
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<223> 1 of 2 allelic variants (1470 is other entry)  
  
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<223> Accession number cg29498780  
  
<400> 1469  
agaggagacc acagaagccc cgacgttgca cagccctgca ggcaggggct g 51  
  
<210> 1470  
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<223> Accession number cg29498780  
  
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<210> 1471  
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<213> Homo sapiens  
  
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<223> 1 of 2 allelic variants (1472 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29513153  
  
<400> 1471  
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<210> 1472  
<211> 51  
<212> DNA  
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<223> Accession number cg29513153

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<210> 1473  
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<220>  
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<223> 1 of 2 allelic variants (1474 is other entry)

<221> misc\_feature  
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gcggcaggaa cctgccactc ctgggagcaa aaagctgctc tcgggaaccc t 51

<210> 1474  
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<221> misc\_feature  
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<400> 1474  
gcggcaggaa cctgccactc ctgggggcaa aaagctgctc tcgggaaccc t 51

<210> 1475  
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<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg29514688

<400> 1475  
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<210> 1476  
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<210> 1477  
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<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1478 is other entry)

<221> misc\_feature  
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<400> 1477  
gggtttcgcc atgttgccca ggctggtctt gaactcctgg gctcgagtga t 51

<210> 1478  
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<221> misc\_feature  
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<223> Accession number cg29514688

<400> 1478  
gggtttcgcc atgttgccca ggctggtctt gaactcctgg gctcgagtga t 51

<210> 1479  
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<221> misc\_feature  
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cttgaactcc tgggctcgag tgatccacct gcctcagcct cccaatgcgc t 51

<210> 1480  
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cttgaactcc tgggctcgag tgatctacct gcctcagcct cccaatgcgc t 51

<210> 1481  
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<220>  
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<223> 1 of 2 allelic variants (1482 is other entry)

<221> misc\_feature  
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<223> Accession number cg29689883

<400> 1481  
ggccactttt cttttctctg ttttgttttt ttttctttt tttcttttt t 51

<210> 1482  
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<220>

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<210> 1483  
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<221> misc\_feature  
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<210> 1484  
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<400> 1484  
tttttttctt tttttctttt tttttcttct ctttttgaga cattctcact 50

<210> 1485  
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<213> Homo sapiens

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<221> misc\_feature  
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<223> Accession number cg29692482

<400> 1485  
tttctctccac ctccctccac tcattcaggt caggcatcga atgtcacttt c 51

<210> 1486  
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<220>  
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<223> 2 of 2 allelic variants (1485 is other entry)

<221> misc\_feature  
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<400> 1486  
tttctctccac ctccctccac tcatttaggt caggcatcga atgtcacttt c 51

<210> 1487  
<211> 44  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1488 is other entry)

<221> misc\_feature  
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<223> Accession number cg29694531

<400> 1487  
ttgcaaaaat aacccttgg ggctctgtct cctcaacta ttgc 44

<210> 1488  
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<212> DNA  
<213> Homo sapiens

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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg29694531

<400> 1488  
ttgcaaaaat aacccttgg gctctgtctc cctcaactat tgc

43

<210> 1489  
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<221> misc\_feature  
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<223> Accession number cg29694531

<400> 1489  
ttgcaaaaat aacccttgg ggctctgtct cctcaacta ttgtct

47

<210> 1490  
<211> 46  
<212> DNA  
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<223> Nucleotide deleted between bases 21 and 22

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg29694531

<400> 1490  
ttgcaaaaat aacccttgg gctctgtctc cctcaactat tgcct

46

<210> 1491  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1492 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg29694613

<400> 1491

agtaggtatc cccgctcccc caccaacccc caatttgaat gcacatttga

50

<210> 1492

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1491 is other entry)

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<222> (0)...(0)

<223> Accession number cg29694613

<400> 1492

agtaggtatc cccgctcccc caccacaccc ccaatttgaa tgcacatttg a

51

<210> 1493

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1494 is other entry)

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<222> (0)...(0)

<223> Accession number cg29694613

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51

<210> 1494

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1493 is other entry)

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<400> 1494  
tccagtgttt ttcagtaggt atccctgctc cccaccaac cccaatttg a

51

<210> 1495  
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<221> misc\_feature  
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<400> 1495  
gttgacgtga gccgagatcg tgcactgca ctccagcctg ggtgacagag c

51

<210> 1496  
<211> 51  
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<221> misc\_feature  
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<400> 1496  
gttgacgtga gccgagatcg tgccattgca ctccagcctg ggtgacagag c

51

<210> 1497  
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<223> 1 of 2 allelic variants (1498 is other entry)

<221> misc\_feature  
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<223> Accession number cg29970826

<400> 1497  
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51

<210> 1498

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1497 is other entry)

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<223> Accession number cg29970826

<400> 1498

gtttgtcctg gcacggaaca ggagatatac gtaagcagct aagtctcttc c

51

<210> 1499

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1500 is other entry)

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<222> (0)...(0)

<223> Accession number cg29970826

<400> 1499

ctaagtctct tccaaggaac ggtggagaca ccaatcacca tgtcgaggtg a

51

<210> 1500

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1499 is other entry)

<221> misc\_feature

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<223> Accession number cg29970826

<400> 1500

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51

<210> 1501

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1502 is other entry)

<221> misc\_feature  
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<223> Accession number cg30123222

<400> 1501  
ctatgacatg acactattac attttggttt ttagcatttt taaagaggaa g 51

<210> 1502  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg30123222

<400> 1502  
ctatgacatg acactattac attttagttt ttagcatttt taaagaggaa g 51

<210> 1503  
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<221> misc\_feature  
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<400> 1503  
cccgcggaaca agtcaagatc tgtgatttgg cgtcagtggc aacctagttg 50

<210> 1504  
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<220>  
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<222> (26)...(0)  
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<221> misc\_feature  
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<400> 1504  
cccgcggaca agtcaagatc tgtgattttg gcgtcagtgg caacctagtt g 51

<210> 1505  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg30144940

<400> 1505  
catccatcgc gacgtcaaac cgaccgatat cttgggtcaac acccgcggaac a 51

<210> 1506  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg30144940

<400> 1506  
catccatcgc gacgtcaaac cgaccaatat cttgggtcaac acccgcggaac a 51

<210> 1507  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1508 is other entry)

<221> misc\_feature  
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<223> Accession number cg30148429

<400> 1507  
atgacagaaa tgctacagta agggagagga gatgggggaa ggcaaaaggg g 51

<210> 1508  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1507 is other entry)

<221> misc\_feature  
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<400> 1508  
atgacagaaa tgctacagta agggacagga gatgggggaa ggcaaaaggg g 51

<210> 1509  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1510 is other entry)

<221> misc\_feature  
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<223> Accession number cg30148429

<400> 1509  
agtaaggagg agggatggg ggaaggcaaa aggggggttc tacttattaa g 51

<210> 1510  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1510  
agtaaggagg agggatggg ggaagacaaa aggggggttc tacttattaa g 51

<210> 1511  
<211> 51

<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 1511  
ggagatgggg gaaggcaaaa ggggggttcct acttattaag tcaaatagat c

51

<210> 1512  
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<221> misc\_feature  
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<400> 1512  
ggagatgggg gaaggcaaaa ggggggttcct acttattaag tcaaatagat c

51

<210> 1513  
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<223> 1 of 2 allelic variants (1514 is other entry)

<221> misc\_feature  
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<223> Accession number cg30154402

<400> 1513  
tatgtgaagt aaaacaaaaa caaaagttgt tacaattttt tcccttctaa t

51

<210> 1514  
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<220>  
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<223> 2 of 2 allelic variants (1513 is other entry)

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<223> Accession number cg30154402

<400> 1514

tatgtgaagt aaaacaaaaa caaaacttgt tacaattttt tcccttctaa t

51

<210> 1515

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1516 is other entry)

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<223> Accession number cg30177428

<400> 1515

gtgtgagggt gcaggttctc cccaagggcc cattttctgc accagaaagc t

51

<210> 1516

<211> 50

<212> DNA

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30177428

<400> 1516

gtgtgagggt gcaggttctc cccaaggccc attttctgca ccagaaagct

50

<210> 1517

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1518 is other entry)

<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg30179644

<400> 1517  
ccttttggtgg ggagaagtga aaaaagagga tctgaagact cattagttgt 50

<210> 1518  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg30179644

<400> 1518  
ccttttggtgg ggagaagtga aaaaagagg atctgaagac tcattagttg t 51

<210> 1519  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg30275403

<400> 1519  
gtgggcagca ggaattggga ggaggaggtg ggggtggggc acagagcggg g 51

<210> 1520  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30275403

<400> 1520

gtgggcagca ggaattggga ggaggggtgg ggggtggggca cagagcgggg

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<210> 1521

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1522 is other entry)

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<222> (0)...(0)

<223> Accession number cg30373246

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51

<210> 1522

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1521 is other entry)

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<223> Accession number cg30373246

<400> 1522

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51

<210> 1523

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1524 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30386365

<400> 1523  
gaccccgatt aggcagctca gggtattatt gcagcttgat ggcacctggg a 51

<210> 1524  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> Accession number cg30386365

<400> 1524  
gaccccgatt aggcagctca gggtactatt gcagcttgat ggcacctggg a 51

<210> 1525  
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<220>  
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<223> 1 of 2 allelic variants (1526 is other entry)

<221> misc\_feature  
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<400> 1525  
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<210> 1526  
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<220>  
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<221> misc\_feature  
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<400> 1526  
aggcttcacc tcctcagtgg gctaggtgca attctaacca gggggcaagt t 51

<210> 1527  
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<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (1528 is other entry)

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<222> (0)...(0)

<223> Accession number cg30420313

<400> 1527

agtacaataa tgacccgcac cagggcacag ctgaaatggc actgactgat a

51

<210> 1528

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1527 is other entry)

<221> misc\_feature

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<223> Accession number cg30420313

<400> 1528

agtacaataa tgacccgcac caggggacag ctgaaatggc actgactgat a

51

<210> 1529

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1530 is other entry)

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<223> Accession number cg30421261

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51

<210> 1530

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1529 is other entry)

<221> misc\_feature  
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<223> Accession number cg30421261

<400> 1530  
tagtccccctt ctttgtcaac gctttcatgt tctgggtagt ggacaatttc c

51

<210> 1531  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1532 is other entry)

<221> misc\_feature  
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<223> Accession number cg30421963

<400> 1531  
aggcactgtc ccttgctgcc ttcccagaca acctgtaccc tccaggccac c

51

<210> 1532  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1531 is other entry)

<221> misc\_feature  
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<223> Accession number cg30421963

<400> 1532  
aggcactgtc ccttgctgcc ttcccggaca acctgtaccc tccaggccac c

51

<210> 1533  
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<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1534 is other entry)

<221> misc\_feature  
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<223> Accession number cg30453852

<400> 1533

cggtgcttg attcctttga tgaaaaggca aagccttgaa cctaagtcac c 51

<210> 1534  
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<221> misc\_feature  
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cggtgcttg attcctttga tgaaaggga aagccttgaa cctaagtcac c 51

<210> 1535  
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<221> misc\_feature  
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<223> Accession number cg30489596

<400> 1535  
aataagtata gcaagtttat aaaggaaaaa gataaaatac agttccagta t 51

<210> 1536  
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aataagtata gcaagtttat aaaggaaaaa gataaaatac agttccagta t 51

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<220>  
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gcctttaatc ctgggagata aagccaagat ctctgagttc aaggccagca t 51

<210> 1538  
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<400> 1538  
gcctttaatc ctgggagata aagccgagat ctctgagttc aaggccagca t 51

<210> 1539  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1540 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30490648

<400> 1539  
acaggtacag cctgcggtca gacacaacca caaggcacat gaactcccca g 51

<210> 1540  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1539 is other entry)



<221> misc\_feature  
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<223> Accession number cg30490648

<400> 1540  
acaggtacag cctgcggtca gacacgacca caaggcacat gaactcccca g 51

<210> 1541  
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<212> DNA  
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<223> 1 of 2 allelic variants (1542 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30575906

<400> 1541  
ttttctcggg aaatggtcct aaaatgaaac ctggcggttta acatggacac t 51

<210> 1542  
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<220>  
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<221> misc\_feature  
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<400> 1542  
ttttctcggg aaatggtcct aaaataaaac ctggcggttta acatggacac t 51

<210> 1543  
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<220>  
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<223> 1 of 2 allelic variants (1544 is other entry)

<221> misc\_feature  
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<223> Accession number cg30578763

<400> 1543  
gaggtctcggg tcgggttcgc catgtgaggg gcaagaggtg tctgccccct c 51

<210> 1544  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
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<221> misc\_feature  
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<223> Accession number cg30578763  
  
<400> 1544  
gaggtctggt tcgggttcgc catgtaagg gcaagaggtg tctgccccct c 51  
  
<210> 1545  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
<220>  
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<223> 1 of 2 allelic variants (1546 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30630643  
  
<400> 1545  
gttcttggt gggggttaga tgactgcaag aattgggtct gtatttaata a 51  
  
<210> 1546  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1545 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30630643  
  
<400> 1546  
gttcttggt gggggttaga tgactccaag aattgggtct gtatttaata a 51  
  
<210> 1547  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1548 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30748852

<400> 1547  
aaccagggaa cattatggcc tgaggcccca gaggagtggg acagttacc a 51

<210> 1548  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1547 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30748852

<400> 1548  
aaccagggaa cattatggcc tgaggccag aggagtggga cagttaccca 50

<210> 1549  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1550 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30749846

<400> 1549  
ggtcgagcag ggttttactt ttagttggat ctgtcgtgtg acttgctct a 51

<210> 1550  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 2 of 2 allelic variants (1549 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30749846

<400> 1550  
ggtcgagcag ggttttactt ttagtgggat ctgtcgtgtg acttgctct a 51

<210> 1551  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1552 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30750319

<400> 1551  
ggcttactcc ttgatggaa agtggggaca aaaggctaga gtgcagcagt t 51

<210> 1552  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1551 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30750319

<400> 1552  
ggcttactcc ttgatggaa agtggagaca aaaggctaga gtgcagcagt t 51

<210> 1553  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1554 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30750319

<400> 1553  
agcatcagtgtgtgcccccgagcccaggccttgccaccccagAACAGATAGG a 51

<210> 1554  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1553 is other entry)

<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30750319

<400> 1554  
agcatcagtgtgtgcccccgagcccaggccttgccaccccagAACAGATAGG a 50

<210> 1555  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1556 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30750659

<400> 1555  
aggactaaatgtaagagagaggggatagcaagccttgaggaaagaaactc c 51

<210> 1556  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1555 is other entry)

<221> misc\_feature  
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<223> Accession number cg30750659

<400> 1556

aggactaaat gtaagagaga gggatggcaa agcttgagga aaagaaactc c

51

<210> 1557

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1558 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30750659

<400> 1557

taggaccca tgcctcaaat cgctcaacac ccaccctga ctctgaaaat c

51

<210> 1558

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1557 is other entry)

<221> misc\_feature

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<223> Accession number cg30750659

<400> 1558

taggaccca tgcctcaaat cgctcgacac ccaccctga ctctgaaaat c

51

<210> 1559

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1560 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30783885

<400> 1559

gcggcccaga accttggggc cggtactca ctggggcatt ggctgcatac c

51

<210> 1560

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1559 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30783885

<400> 1560  
gcggcccaga accttgggcc cggctgctca ctggggcatt ggctgcatac c 51

<210> 1561  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1562 is other entry)

<221> misc\_feature  
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<223> Accession number cg30783885

<400> 1561  
aaccttgggc cggctactc actggggcat tggctgcata cctgaccac g 51

<210> 1562  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1561 is other entry)

<221> misc\_feature  
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<223> Accession number cg30783885

<400> 1562  
aaccttgggc cggctactc actggagcat tggctgcata cctgaccac g 51

<210> 1563  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1564 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30784771

<400> 1563  
tttatttcta tagaacaaaa aaaaaagtta agagattagt agagacgggt c 51

<210> 1564  
<211> 50  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30784771

<400> 1564  
tttatttcta tagaacaaaa aaaaagttaa gagattagta gagacgggtc 50

<210> 1565  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1566 is other entry)

<221> misc\_feature  
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<223> Accession number cg30785174

<400> 1565  
cgtttctctg gtttttctgg tctccgaaat tcaaggattt ctacagttag c 51

<210> 1566  
<211> 51  
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<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1565 is other entry)

<221> misc\_feature  
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<223> Accession number cg30785174

<400> 1566

cgtttctctg gtttttctgg tctccaaaat tcaaggattt ctacagttag c

51

<210> 1567

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1568 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30785603

<400> 1567

aagttccctt agctgagaac caaagaagtg gtcccgactg tgcaggcagc t

51

<210> 1568

<211> 50

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1567 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30785603

<400> 1568

aagttccctt agctgagaac caaagagtgg tcccgactgt gcaggcagct

50

<210> 1569

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1570 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30785603

<400> 1569  
agttccccta gctgagaacc aaagaagtgg tcccgactgt gcaggcagct t 51

<210> 1570  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1569 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30785603

<400> 1570  
agttccccta gctgagaacc aaagagtggg cccgactgtg caggcagctt 50

<210> 1571  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1572 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30785603

<400> 1571  
caaagaagtg gtcccgactg tgcaggcagc ttgaaagaag aaacaggccc g 51

<210> 1572  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1571 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30785603

<400> 1572  
caaagaagtg gtcccgactg tgcagccagc ttgaaagaag aaacaggccc g 51

<210> 1573  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1574 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30785957

<400> 1573  
ttcgcgaaatg tgtgtgtggc ataccttggc cccatcgtct gtcccataat c

51

<210> 1574  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1573 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30785957

<400> 1574  
ttcgcgaaatg tgtgtgtggc ataccctggc cccatcgtct gtcccataat c

51

<210> 1575  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1576 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30786264

<400> 1575  
ctcaaaccct ttgaactcct cagtgggtcc ctcccccatg cagctgtact c

51

<210> 1576  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1575 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30786264

<400> 1576  
ctcaaaccct ttgaactcct cagtgattcc ctcccccatg cagctgtact c 51

<210> 1577  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1578 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30786450

<400> 1577  
tcacagcagc caattctttc tcccttagcc tcacgcggtt ccagtcagcc t 51

<210> 1578  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1577 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30786450

<400> 1578  
tcacagcagc caattctttc tccctcagcc tcacgcggtt ccagtcagcc t 51

<210> 1579  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1580 is other entry)

<221> misc\_feature

<222> (25)...(26)  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30787589

<400> 1579  
cgtctggagc cttctttttt tttttgagac aggatctcgc tccgtcctcc 50

<210> 1580  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1579 is other entry)

<221> misc\_feature  
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<223> Accession number cg30787589

<400> 1580  
cgtctggagc cttctttttt tttttgaga caggatctcg ctccgtcctc c 51

<210> 1581  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1582 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30787589

<400> 1581  
cgtctggagc cttctttttt tttttgagac aggatctcgc tccgtcctcc 50

<210> 1582  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1581 is other entry)

<221> misc\_feature  
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<223> Accession number cg30787589

<400> 1582  
cgtctggagc cttctttttt ttttttgaga caggatctcg ctccgtcctc c 51

<210> 1583  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1584 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30787705

<400> 1583  
gagtaacacc ctttttcaaa aaaaaagtta ccattttctg taataggaaa a 51

<210> 1584  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1583 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30787705

<400> 1584  
gagtaacacc ctttttcaaa aaaaagttac cattttctgt aataggaaaa 50

<210> 1585  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1586 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg30787705

<400> 1585  
aaatgtgaaa gactctttag gacaaaatac caagtggaaa gaacaggaat a 51

<210> 1586  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1585 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30787705

<400> 1586  
aaatgtgaaa gactctttag gacaatatac caagtggaaa gaacaggaat a 51

<210> 1587  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1588 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30787816

<400> 1587  
taaaaacatc actcttggag ctgcaggga aaggagttga gaagcatgga a 51

<210> 1588  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1587 is other entry)

<221> misc\_feature  
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<223> Accession number cg30787816

<400> 1588  
taaaaacatc actcttggag ctgcatggaa aaggagttga gaagcatgga a 51

<210> 1589  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1590 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30788422

<400> 1589  
gattgcatgg aggcccgcc cccccaacc aattcttga taatgcaca g

51

<210> 1590  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1589 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg30788422

<400> 1590  
gattgcatgg aggcccgcc cccccaacca attctttgat aatgcacag

50

<210> 1591  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1592 is other entry)

<221> misc\_feature  
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51

<210> 1592  
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<212> DNA  
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<223> 2 of 2 allelic variants (1591 is other entry)

<221> misc\_feature  
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51

<210> 1593  
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<400> 1593  
gtcctgggca ggaagatgag gcaaacacaa gcacatggat gcacgcacac a

51

<210> 1594  
<211> 51  
<212> DNA  
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<221> misc\_feature  
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<223> Accession number cg30790895

<400> 1594  
gtcctgggca ggaagatgag gcaaatacaa gcacatggat gcacgcacac a

51

<210> 1595  
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<223> 1 of 2 allelic variants (1596 is other entry)

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<223> Accession number cg30790895

<400> 1595

caggaagatg aggcaaacac aagcacatgg atgcacgcac acactcgtgc t

51

<210> 1596

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1595 is other entry)

<221> misc\_feature

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<223> Accession number cg30790895

<400> 1596

caggaagatg aggcaaacac aagcaaattg atgcacgcac acactcgtgc t

51

<210> 1597

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (1598 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30792591

<400> 1597

ttgatattg gctttaaaat gttttcattt aataccccct cccccacaca c

51

<210> 1598

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30792591

<400> 1598  
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<210> 1599  
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<223> Accession number cg30793374

<400> 1599  
aattgaactg ctgttccttg tgtgccgggc cccatagcta gcactgggaa c 51

<210> 1600  
<211> 51  
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<221> misc\_feature  
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<400> 1600  
aattgaactg ctgttccttg tgtgctgggc cccatagcta gcactgggaa c 51

<210> 1601  
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<223> 1 of 2 allelic variants (1602 is other entry)

<221> misc\_feature  
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<223> Accession number cg30794324

<400> 1601  
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<210> 1602  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1601 is other entry)

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<223> Accession number cg30794324

<400> 1602

tcctaaatga gtgttttagaa tagttgtttc attggaaaca aggtcaaaac a

51

<210> 1603

<211> 45

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1604 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30794324

<400> 1603

tctaccacaa ttatttgatc aactagttat caaccctgac tgcag

45

<210> 1604

<211> 45

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg30794324

<400> 1604

tctaccacaa ttatttgatc aactaattat caaccctgac tgcag

45

<210> 1605

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1606 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32073644

<400> 1605  
accctcctgg cacatctctg ctcaccctgc gagcaaccga ccccgacgtg g

51

<210> 1606  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg32073644

<400> 1606  
accctcctgg cacatctctg ctcactctgc gagcaaccga ccccgacgtg g

51

<210> 1607  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1608 is other entry)

<221> misc\_feature  
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<223> Accession number cg32119723

<400> 1607  
tggatcgcca gggctacggc cagatcaagg tggtcgcgc cgatggggac a

51

<210> 1608  
<211> 51  
<212> DNA  
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<223> 2 of 2 allelic variants (1607 is other entry)

<221> misc\_feature  
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<400> 1608

tggatcgcca gggctacggc cagattaagg tggccgcgc cgatggggac a

51

<210> 1609

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1610 is other entry)

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<222> (0)...(0)

<223> Accession number cg32119813

<400> 1609

gcccgtcgta cgtggggcgc tcgcgctggg tgcagacgcg cttgattggt t

51

<210> 1610

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1609 is other entry)

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<222> (0)...(0)

<223> Accession number cg32119813

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gcccgtcgta cgtggggcgc tcgcggtggg tgcagacgcg cttgattggt t

51

<210> 1611

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1612 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg32120097

<400> 1611

tggcctgcac gtccgcacg ctcagctccc gctggccccg gctgtacagg a

51

<210> 1612

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg32120097

<400> 1612  
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<210> 1613  
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<212> DNA  
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<223> 1 of 2 allelic variants (1614 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32126043

<400> 1613  
cctgtggcat ccgttctgat ggaaacgtgc agttgtattt ggaagttcag a 51

<210> 1614  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> Accession number cg32126043

<400> 1614  
cctgtggcat ccgttctgat ggaaatgtgc agttgtattt ggaagttcag a 51

<210> 1615  
<211> 51  
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<213> Homo sapiens

<220>

<221> misc\_feature  
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<223> 1 of 2 allelic variants (1616 is other entry)

<221> misc\_feature  
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<223> Accession number cg32149436

<400> 1615  
agggcgcccc gagtggctcc aggaacgacg gaaaccctc agggcttttg g 51

<210> 1616  
<211> 51  
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<221> misc\_feature  
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<400> 1616  
agggcgcccc gagtggctcc aggaaggacg gaaaccctc agggcttttg g 51

<210> 1617  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg32149517

<400> 1617  
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<210> 1618  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (1617 is other entry)

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<400> 1618  
tgtgcgtgta tgtgcgcttg ctctgtcatg cgtgggtgtgt gtatgtgtgt g 51

<210> 1619  
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tgggtggtgtc gccagagagt gacctgcctg tctgggggtgg aggaaaagcc a 51

<210> 1620  
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<220>  
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<400> 1620  
tggtggtgtc gccagagagt gacctccctg tctgggggtgg aggaaaagcc a 51

<210> 1621  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg32150747

<400> 1621  
cagaacttcg gcagtaaaga ataaaaggcc agacagagag gcagcagcac a 51

<210> 1622  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 1622  
cagaacttcg gcagtaaaga ataaaggcca gacagagagg cagcagcaca 50

<210> 1623  
<211> 51  
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<220>  
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<223> 1 of 2 allelic variants (1624 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32152942

<400> 1623  
cacagctgtg catgtcgact taggtggcct gccagctcat ctccggcggc a 51

<210> 1624  
<211> 51  
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<400> 1624  
cacagctgtg catgtcgact taggtagcct gccagctcat ctccggcggc a 51

<210> 1625  
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<221> misc\_feature  
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<400> 1625  
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<210> 1626  
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ggtggcctgc cagctcatct ccggcagcac ggtcaacgac gtcgagctgc c 51

<210> 1627  
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<221> misc\_feature  
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ggcctgccag ctcctctccg gcggcacggt caacgacgac gagctgccgc g 51

<210> 1628  
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<220> .  
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<221> misc\_feature  
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<400> 1628  
ggcctgccag ctcacatctcgc gcggcccggt caacgacgtc gagctgccgc g 51

<210> 1629  
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<221> misc\_feature  
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<400> 1629  
tcacttggtc agattggcca tggatagtca cctgatcccc aacgatgtgg g 51

<210> 1630  
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<400> 1630  
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<210> 1631  
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<220>  
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<221> misc\_feature

<222> (0)...(0)  
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<210> 1632  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg32152942

<400> 1632  
ggccatggat agtcacctga tccccgacga tgtgggctag ctgactagcg g 51

<210> 1633  
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<221> misc\_feature  
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tcacctgatc cccaacgatg tgggctagct gactagcggt aacttgagct c 51

<210> 1634  
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<221> misc\_feature  
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<400> 1634  
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<210> 1635  
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<223> Accession number cg32152942  
  
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<210> 1636  
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<213> Homo sapiens  
  
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<223> 1 of 2 allelic variants (1638 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32153241  
  
<400> 1637  
accgggctcc ggtcccgagg tccacagca gttgaccagg catgggccgc a 51  
  
<210> 1638  
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<213> Homo sapiens  
  
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<221> misc\_feature  
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<223> 2 of 2 allelic variants (1637 is other entry)

<221> misc\_feature  
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<223> Accession number cg32153241

<400> 1638  
accgggtcc ggtcccgagg tcccatagca gttgaccagg catgggccgc a 51

<210> 1639  
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<220>  
<221> misc\_feature  
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<222> (0)...(0)  
<223> Accession number cg32153241

<400> 1639  
gcatgggccg cagggctgcc agcgcgacag ctcgtaccgc gtgcttggtg a 51

<210> 1640  
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<210> 1641  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<400> 1641

cagctcgtag cgcgtgcttg gtgataagtc cgtcgtgggc gaaatgctcc t

51

<210> 1642

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<212> DNA

<213> Homo sapiens

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cagctcgtag cgcgtgcttg gtgatgagtc cgtcgtgggc gaaatgctcc t

51

<210> 1643

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1644 is other entry)

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<222> (0)...(0)

<223> Accession number cg32153241

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tggtgataag tccgtcgtgg gcgaaatgct cctcggccag gccgggggta c

51

<210> 1644

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1643 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg32153241

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tggtgataag tccgtcgtgg gcgaagtgct cctcggccag gccgggggta c

51

<210> 1645



<211> 51  
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<220>  
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<223> 1 of 2 allelic variants (1646 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32158391

<400> 1645  
tgcataccat gctccagagg aagcagataa atctgaccc t aaacctgggg t 51

<210> 1646  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1645 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32158391

<400> 1646  
tgcataccat gctccagagg aagcaataaa tctgaccta aacctgggg t 50

<210> 1647  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1648 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32168122

<400> 1647  
catgcgcgct ggcctccatg ggtggcgga cgcactgtg gacgcacttg c 51

<210> 1648  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 2 of 2 allelic variants (1647 is other entry)

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<222> (0)...(0)

<223> Accession number cg32168122

<400> 1648

catgcgcgct ggcctccatg ggtgggggga ccgactgtgt gacgcacttg c

51

<210> 1649

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1650 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg32168828

<400> 1649

tgattcgccg cacaggtcgt ttagggcaac gccaaagttcg aagacgtccc c

51

<210> 1650

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1649 is other entry)

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<223> Accession number cg32168828

<400> 1650

tgattcgccg cacaggtcgt ttaggacaac gccaaagttcg aagacgtccc c

51

<210> 1651

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1652 is other entry)

<221> misc\_feature  
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<223> Accession number cg32177197

<400> 1651  
caccgtgttg ccgaaaaggt cgctcacctc taccacgata cggtgggtac c 51

<210> 1652  
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<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1651 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32177197

<400> 1652  
caccgtgttg ccgaaaaggt cgctcgctc taccacgata cggtgggtac c 51

<210> 1653  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1654 is other entry)

<221> misc\_feature  
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<223> Accession number cg32177197

<400> 1653  
ggggaaggaa tggaaagcgg tggggtcgta ggtcgtcggg gcagtgcctc a 51

<210> 1654  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1653 is other entry)

<221> misc\_feature  
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<400> 1654

ggggaaggaa tggaaagcgg tggggccgtc ggtcgtcggg gcagtgcccc a

51

<210> 1655

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (20)...(0)

<223> 1 of 2 allelic variants (1656 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg32177584

<400> 1655

ccgcacgcgt gagccaccgt gcctggccca cgtgacactg ttaaa

45

<210> 1656

<211> 45

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1655 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg32177584

<400> 1656

ccgcacgcgt gagccaccgc gcctggccca cgtgacactg ttaaa

45

<210> 1657

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1658 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg32180618

<400> 1657

aatcagcacg gtgcgcgtga ggggcgggcg cgcttctcac acatgctgtg c

51

<210> 1658

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1657 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32180618

<400> 1658  
aatcagcacg gtgcgcgtga ggggcaggcg cgcttctcac acatgctgtg c 51

<210> 1659  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1660 is other entry)

<221> misc\_feature  
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<223> Accession number cg32195480

<400> 1659  
cctttccctt gcgtacactc tggactccag gcaggaaaat caaggcctca c 51

<210> 1660  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1659 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32195480

<400> 1660  
cctttccctt gcgtacactc tggaccccag gcaggaaaat caaggcctca c 51

<210> 1661  
<211> 50  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1662 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32195480

<400> 1661  
gcattagtcc aggacagcag acccctctgg acgctgactc gggatggggt 50

<210> 1662  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1661 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32195480

<400> 1662  
gcattagtcc aggacagcag acccctctg gacgctgact cgggatgggg t 51

<210> 1663  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1664 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32308743

<400> 1663  
tttccgtacg cgtgaacgtc tgtgttgtct gtggaatccc ctggggacgt t 51

<210> 1664  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1663 is other entry)

<221> misc\_feature  
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<223> Accession number cg32308743

<400> 1664

tttccgtacg cgtgaacgtc tgtgtcgtct gtggaatccc ctcgggacgt t

51

<210> 1665

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1666 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg32338390

<400> 1665

gagccataag ggaggacttg gcagcgtgct tgctccctga gtgacgttgt g

51

<210> 1666

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1665 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg32338390

<400> 1666

gagccataag ggaggacttg gcagcatgct tgctccctga gtgacgttgt g

51

<210> 1667

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1668 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg32544064

<400> 1667

caggagtcca tgaccagcct ggccaacaca gtgagacccc gtctctacta a

51

<210> 1668

<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1667 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32544064

<400> 1668  
caggagtcca tgaccagcct ggccagcaca gtgagacccc gtctctacta a 51

<210> 1669  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1670 is other entry)

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<223> Accession number cg32544064

<400> 1669  
gagttcatga ccagcctggc caacacagtg agaccccgtc tctactaaaa a 51

<210> 1670  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1669 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg32544064

<400> 1670  
gagttcatga ccagcctggc caacatagtg agaccccgtc tctactaaaa a 51

<210> 1671  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature



<222> (26)...(0)  
<223> 1 of 2 allelic variants (1672 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33193895

<400> 1671  
tctctcctnt gccaaagataa aaataatatt ctocctgggc tttcttaact a 51

<210> 1672  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1671 is other entry)

<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33193895

<400> 1672  
tctctcctnt gccaaagataa aaatatattc tccttgggct ttcttaacta 50

<210> 1673  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1674 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33193895

<400> 1673  
tctcctntgc caagataaaa ataatatctt ccctgggctt tcttaactac a 51

<210> 1674  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1673 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33193895

<400> 1674  
tctcctntgc caagataaaa ataatttctc cctgggcttt cttaactaca 50

<210> 1675  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1676 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33194116

<400> 1675  
gtgtcactag tgtgaaaaaa gttgtagtgg agagcttggt atgtcaggca a 51

<210> 1676  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1675 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33194116

<400> 1676  
gtgtcactag tgtgaaaaaa gttgtgtgga gagcttggtgta tgtcaggcaa 50

<210> 1677  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 1 of 2 allelic variants (1678 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33199608

<400> 1677  
gattctcctg tctcaacctg ccaagtagct gggactacag gcgcacgccca c 51

<210> 1678  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1677 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33199608

<400> 1678  
gattctcctg tctcaacctg ccaagcagct gggactacag gcgcacgccca c 51

<210> 1679  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1680 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33199608

<400> 1679  
cgccaccacg accggccaat ttctgcactt ttagtagaga cagggttca c 51

<210> 1680  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1679 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33199608

<400> 1680  
cgccaccacg accggccaat ttctgtactt ttagtagaga cagggcttca c 51

<210> 1681  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1682 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33208319

<400> 1681  
ccttgatgag gctgtctttt aagctcaatt gaaggtagta acaacaatcc t 51

<210> 1682  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1681 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33208319

<400> 1682  
ccttgatgag gctgtctttt aagcttaatt gaaggtagta acaacaatcc t 51

<210> 1683  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1684 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33208319

<400> 1683  
gaaatgtgta gattctggaa cagtgccctag caggttgcag atacttacta g 51

<210> 1684  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1683 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33208319

<400> 1684  
gaaatgtgta gattctggaa cagtgtctag caggttgcag atacttacta g

51

<210> 1685  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1686 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33208319

<400> 1685  
aagttttctg agtgaatgaa aagtcacaaa tgaatgtatc cttccaagca t

51

<210> 1686  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1685 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33208319

<400> 1686  
aagttttctg agtgaatgaa aagtcgaaaa tgaatgtatc cttccaagca t

51

<210> 1687  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)

<223> 1 of 2 allelic variants (1688 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg33265890

<400> 1687

tcgtgcttgg aatcagcagg cagggccact tccctcttga agtcacatc t

51

<210> 1688

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 2 of 2 allelic variants (1687 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg33265890

<400> 1688

tcgtgcttgg aatcagcagg cagggccactt ccctcttgaa gtcacatct

50

<210> 1689

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1690 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg33271693

<400> 1689

gttcgggaga aagctacgac caagtacgcc cagctcgggc cttagaactt c

51

<210> 1690

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1689 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33271693

<400> 1690  
gttcgggaga aagctacgac caagtcgccc agctcgggcc ttagaacttc 50

<210> 1691  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1692 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33899283

<400> 1691  
cccttcggga ttggagtctg acctgaaagc atggataatt attcacattt c 51

<210> 1692  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1691 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg33899283

<400> 1692  
cccttcggga ttggagtctg acctgtaagc atggataatt attcacattt c 51

<210> 1693  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1694 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg34078594

<400> 1693

agagacaagg cttcctcata ggacggcaga gccaccttta ggaacagctt g

51

<210> 1694

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1693 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34078594

<400> 1694

agagacaagg cttcctcata ggacgcagag ccacctttag gaacagcttg

50

<210> 1695

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1696 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34078594

<400> 1695

tcaaagtga gaagcaggag gcggggagtt ccgcctctcc cagcccaagg g

51

<210> 1696

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1695 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34078594



<400> 1696  
tcaaagtgaa gaagcaggag gcgggcagtt ccgcctctcc cagcccaagg g 51

<210> 1697  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1698 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34078713

<400> 1697  
tgaaaatagt gtgctgagcc ctggaacatt aaaaatgtgt tcctatgtgg a 51

<210> 1698  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1697 is other entry)

<221> misc\_feature  
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<223> Accession number cg34078713

<400> 1698  
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<210> 1699  
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<400> 1699  
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<210> 1700  
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (1699 is other entry)

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<223> Accession number cg34096681

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51

<210> 1701

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1702 is other entry)

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<223> Accession number cg34098766

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<210> 1702

<211> 50

<212> DNA

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50

<210> 1703

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<212> DNA

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<223> Accession number cg34098766  
  
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<210> 1707  
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<210> 1708  
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<210> 1709  
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<221> misc\_feature  
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<210> 1712  
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<221> misc\_feature  
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<400> 1712

atgctaggaa gctagctcct gggggattca gatctagtga gggcgcttt c

51

<210> 1713

<211> 51

<212> DNA

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34126415

<400> 1713

aagtaaaaac aaacaagata actttttttt ttctgagatg aattttcact t

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<210> 1714

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1716 is other entry)

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<223> Accession number cg34147197

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51

<210> 1716

<211> 51

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<221> misc\_feature  
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<223> Accession number cg34387835

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<210> 1718  
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<210> 1719  
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<210> 1720  
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<210> 1721  
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<221> misc\_feature  
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51



<210> 1723  
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tgccaccaca cccgaccaat ttttgcattt ttagtagaga tgggggttta c

51

<210> 1724  
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<400> 1724  
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51

<210> 1725  
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<221> misc\_feature  
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<223> Accession number cg34405904

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<210> 1728  
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<210> 1729  
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<223> 1 of 2 allelic variants (1730 is other entry)

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<223> Accession number cg34407516

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<210> 1730

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<223> Accession number cg34407516

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<210> 1731

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<223> Accession number cg34407558

<400> 1731

ccaagctcct gcctcgcaat tgcctttgta ggccaagatc atgccgtgaa g

51

<210> 1732

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1731 is other entry)

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<210> 1733  
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<221> misc\_feature  
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51

<210> 1736

<211> 51

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51

<210> 1737

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1738 is other entry)

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51

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ggccaaaatc gtcgtgaagt caccactgc aggcctagct cctgcgtccg a

51

<210> 1739

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<210> 1740  
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<210> 1742  
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<220>  
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<210> 1744  
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<220>  
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<400> 1744  
ctctgcaggc ctagctcctg cgtccaagtg ctgtgtaggc caagctaata c 51

<210> 1745  
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<221> misc\_feature  
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<223> Accession number cg34407558

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<210> 1746  
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<400> 1746  
aagctaattgc ctcacagcac actttcgagg ctgagcggtt ccttttgtgc a 51

<210> 1747  
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<220>  
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<223> 1 of 2 allelic variants (1748 is other entry)

<221> misc\_feature  
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tcacagcaca cttttgaggc tgagcggttc cttttgtgca tcctctccaa g 51

<210> 1748  
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<210> 1749  
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<223> 1 of 2 allelic variants (1750 is other entry)

<221> misc\_feature  
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caagccctga acttactcca gttggcctct ccagaccaag ctctccctcc c 51

<210> 1750  
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<212> DNA  
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<220>  
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caagccctga acttactcca gttggctctet ccagaccaag ctctccctcc c 51

<210> 1751  
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<220>  
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<400> 1751  
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<210> 1752  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1751 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg34409256

<400> 1752  
ttactatata tgatgtagtc taatactttt ctatcctatt ttatttcctt t 51

<210> 1753  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1754 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34409256

<400> 1753  
tatatatgat gtagtctaata aattttctat cctattttat ttcctttttt t 51

<210> 1754  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34409256

<400> 1754  
tatatatgat gtagtctaata aattttctatc ctattttatt ttcctttttt 50

<210> 1755  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1756 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34411960

<400> 1755  
atggtggaga tgcttctggt ttattctgtg gctaccgctg ttactgcttg g 51

<210> 1756  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1755 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34411960

<400> 1756  
atggtggaga tgcttctggt ttatttctgtg gctaccgctg ttactgcttg g 51

<210> 1757  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1758 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34664360

<400> 1757  
agctagacat agagccctga ccgtgtgatt ccaactgtgg aattcacaca a 51

<210> 1758  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1757 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34664360

<400> 1758  
agctagacat agagccctga ccgtgcgatt ccaactgtgg aattcacaca a 51

<210> 1759  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1760 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34750113

<400> 1759  
ttttattggt ttgagacaga gtctcactct gttgcctagg ctggagtgcg g

51

<210> 1760  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (1759 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34750113

<400> 1760  
ttttattggt ttgagacaga gtctcgctct gttgcctagg ctggagtgcg g

51

<210> 1761  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1762 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34750113

<400> 1761  
ggctggagtg cagtgggtgc atcacagctc actgcaactt ccacctcctg g

51

<210> 1762  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)

<223> 2 of 2 allelic variants (1761 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34750113

<400> 1762

ggctggagtg cagtgggtgca atcacggctc actgcaactt ccacctcctg g

51

<210> 1763

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1764 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34888218

<400> 1763

aaatgttggg atcaatatct aaatcgaact ccaaattaca gcctccaggg a

51

<210> 1764

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1763 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34888218

<400> 1764

aaatgttggg atcaatatct aaatcaaact ccaaattaca gcctccaggg a

51

<210> 1765

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1766 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34888218

<400> 1765  
caggctgtat gcctgaagtc cccaagtacc aagtgcattgt actctgctct g 51

<210> 1766  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1765 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34888218

<400> 1766  
caggctgtat gcctgaagtc cccaaatacc aagtgcattgt actctgctct g 51

<210> 1767  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1768 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34888218

<400> 1767  
gaagtcacca agtaccaagt gcatgtactc tgctctgggc taaggatgaa a 51

<210> 1768  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1767 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg34888218

<400> 1768  
gaagtcacca agtaccaagt gcatgcactc tgctctgggc taaggatgaa a 51

<210> 1769  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1770 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34896418

<400> 1769

aaacaaggat taaatctggt cctggtgggt gtatgggata aacatggatt t

51

<210> 1770

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1769 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg34896418

<400> 1770

aaacaaggat taaatctggt cctggcggtt gtatgggata aacatggatt t

51

<210> 1771

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1772 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35001967

<400> 1771

tgagcagaga aactgacct ggtttggcag ggacaggaga tacgctgggt t

51

<210> 1772

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1771 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35001967

<400> 1772  
tgagcagaga acactgacct ggttttgcag ggacaggaga tacgctgggt t 51

<210> 1773  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1774 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35001967

<400> 1773  
agcagagaac actgacctgg tttggcaggg acaggagata cgctggggtt g 51

<210> 1774  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1773 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35001967

<400> 1774  
agcagagaac actgacctgg tttggtaggg acaggagata cgctggggtt g 51

<210> 1775  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1776 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35001967

<400> 1775



agatacgctg ggttggtatg gatcagcaag aggggtactgc taatgggaac a

51

<210> 1776

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1775 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35001967

<400> 1776

agatacgctg ggttggtatg gatcaacaag aggggtactgc taatgggaac a

51

<210> 1777

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1778 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35001967

<400> 1777

aatgggaaca gggagggaag gctcaacccc attcccgat ttcctgatt c

51

<210> 1778

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1777 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35001967

<400> 1778

aatgggaaca gggagggaag gctcacccca ttcccgatt tccctgattc

50

<210> 1779

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1780 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35003947

<400> 1779

tggtctggtg aatgggaact taacatgtct ttgccgttac atattcttg a

51

<210> 1780

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1779 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35003947

<400> 1780

tggtctggtg aatgggaact taacacgtct ttgccgttac atattcttg a

51

<210> 1781

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1782 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35003951

<400> 1781

ttgaactcct gacctcaagt gatccaccg cctcagcctc ctaaagtgt g

51

<210> 1782

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1781 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35003951

<400> 1782  
ttgaactcct gacctcaagt gatccgcccg cctcagcctc ctaaagtgct g 51

<210> 1783  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1784 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35013956

<400> 1783  
cagaatccag ccctgcttga tgcaatcctc ttcagccagg cgttcctgaa t 51

<210> 1784  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1783 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35013956

<400> 1784  
cagaatccag ccctgcttga tgcaaccctc ttcagccagg cgttcctgaa t 51

<210> 1785  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1786 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg35014502

<400> 1785

gagcagtttc tgtttttcta gttaagatgt actgcacatc cccctactgt t

51

<210> 1786

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1785 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35014502

<400> 1786

gagcagtttc tgtttttcta gttaatatgt actgcacatc cccctactgt t

51

<210> 1787

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1788 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35017611

<400> 1787

gcaggcagac gggcagggcc agaggcgcta cgggggtctc ctgcactgta t

51

<210> 1788

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1787 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35017611

<400> 1788  
gcaggcagac gggcagggcc agagggtac cggggtctcc tgcactgtat 50

<210> 1789  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1790 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35019280

<400> 1789  
ataaactgtg tcagacatgg gcgacgcggg gaccgctgga gggaggcgcg c 51

<210> 1790  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1789 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35019280

<400> 1790  
ataaactgtg tcagacatgg gcgaccggg accgctggag ggaggcgcg 50

<210> 1791  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1792 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35019280

<400> 1791  
tccgctggga gcaggagggg cggggccggg cttgaggagt ggctggccgc c 51

<210> 1792  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1791 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35019280

<400> 1792  
tccgctggga gcaggagggg cggggcgggc ttgaggagtg gctggccgcc

50

<210> 1793  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1794 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35023126

<400> 1793  
agaaatacca ttctggacat aagacttggc taaaatttca tgatgaagat a

51

<210> 1794  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1793 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35023126

<400> 1794  
agaaatacca ttctggacat aagacgtggc taaaatttca tgatgaagat a

51

<210> 1795

<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1796 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35049067

<400> 1795  
tctccctgat ggacggggaa gtcttgtttg tggaagacac tgagccacgc t 51

<210> 1796  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1795 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35049067

<400> 1796  
tctccctgat ggacggggaa gtcttctttg tggaagacac tgagccacgc t 51

<210> 1797  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1798 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35049067

<400> 1797  
caccaccacc ggcattccggg gaggagtgtc aaacgggtga ctggccagg a 51

<210> 1798  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 2 of 2 allelic variants (1797 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35049067

<400> 1798  
caccaccacc ggcacccggg gaggactgtc aaacgggtga ctcggccagg a 51

<210> 1799  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1800 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35049067

<400> 1799  
tgcgggcacc ctctgcggg tggacaatga gcgcctggga ggccgttgtc c 51

<210> 1800  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1799 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35049067

<400> 1800  
tgcgggcacc ctctgcggg tggacgatga gcgcctggga ggccgttgtc c 51

<210> 1801  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1802 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35049628



<400> 1801  
gctggaggat tgcttgaagc caggaattca agaccagcct gggcaacata g 51

<210> 1802  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1801 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35049628

<400> 1802  
gctggaggat tgcttgaagc caggagttca agaccagcct gggcaacata g 51

<210> 1803  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1804 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35063579

<400> 1803  
gcagatcact ggaggtcagg agttcaagac cagactggcc aacatggtga a 51

<210> 1804  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1803 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35063579

<400> 1804  
gcagatcact ggaggtcagg agttcgagac cagactggcc aacatggtga a 51

<210> 1805  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1806 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35066497

<400> 1805  
gcgtggcacg cccgtcaggg gcaggtgccc caggggtactc ctacggtgct c 51

<210> 1806  
<211> 51  
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<400> 1806  
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<210> 1807  
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cccagggtag tctacggtg ctcgggcttc ccaccgtggg agtgccgaga c 51

<210> 1808  
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<223> Accession number cg35066497

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51

<210> 1809

<211> 51

<212> DNA

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<210> 1810

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51

<210> 1811

<211> 51

<212> DNA

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<210> 1813  
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<210> 1814  
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caggtatggc attttacgga cagtggggaa gatagacgag ggatggcgct c 51

<210> 1815  
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51

<210> 1816

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1815 is other entry)

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<223> Accession number cg35066497

<400> 1816

ggcctgattc ttgatgtcgt cctggcggtc gctgatggcg tccttggcct t

51

<210> 1817

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (1818 is other entry)

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<223> Accession number cg35068462

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tggcacagga gcccgagatc ttatttcttg acgagccgac aaatcacctt g

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<210> 1818

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<213> Homo sapiens

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<223> 2 of 2 allelic variants (1817 is other entry)

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<400> 1818  
tggcacagga gcccgagatc ttattccttg acgagccgac aaatcacctt g

51

<210> 1819  
<211> 51  
<212> DNA  
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<223> 1 of 2 allelic variants (1820 is other entry)

<221> misc\_feature  
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<223> Accession number cg35072832

<400> 1819  
ttttggataa tatgtaactc tccacaatgt cgcttccgta gcaattgtag a

51

<210> 1820  
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<223> 2 of 2 allelic variants (1819 is other entry)

<221> misc\_feature  
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<223> Accession number cg35072832

<400> 1820  
ttttggataa tatgtaactc tccactatgt cgcttccgta gcaattgtag a

51

<210> 1821  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1822 is other entry)

<221> misc\_feature  
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<223> Accession number cg35074019

<400> 1821

tgcagaagga actggactcg ctgcagggag agaaagtaca cctgaaggag a

51

<210> 1822

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1821 is other entry)

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<223> Accession number cg35074019

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tgcagaagga actggactcg ctgcatggag agaaagtaca cctgaaggag a

51

<210> 1823

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<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1824 is other entry)

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<223> Accession number cg35097790

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tccctcagtt tgctcatctg taaagcagga ataaggctga taccttctca g

51

<210> 1824

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (1823 is other entry)

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<223> Accession number cg35097790

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51

<210> 1825

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1826 is other entry)

<221> misc\_feature  
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<223> Accession number cg35097892

<400> 1825  
gtattttcag tagagacggg gttttaccat gttggccagg ctggtctcga a 51

<210> 1826  
<211> 51  
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<220>  
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<223> Accession number cg35097892

<400> 1826  
gtattttcag tagagacggg gttttgccat gttggccagg ctggtctcga a 51

<210> 1827  
<211> 51  
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<223> 1 of 2 allelic variants (1828 is other entry)

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<223> Accession number cg35098722

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tatgtcttct ttcgttggtt agtggcttgc aggatatttt gacgagcata a 51

<210> 1828  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (1827 is other entry)



<221> misc\_feature  
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<400> 1828  
tatgtcttct ttcggttggt agtgggttgc aggatatttt gagcagcata a 51

<210> 1829  
<211> 51  
<212> DNA  
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<220>  
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<223> Accession number cg35098722

<400> 1829  
ctttcggttg ttagtggtt gcaggatatt ttgagcagca taaaactggt a 51

<210> 1830  
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<223> Accession number cg35098722

<400> 1830  
ctttcggttg ttagtggtt gcagggtatt ttgagcagca taaaactggt a 51

<210> 1831  
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<223> 1 of 2 allelic variants (1832 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35106817

<400> 1831  
atgcaggtgc cgggtgagga cggcaccatg ccgaaactgt tcggacggat c 51

<210> 1832

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1831 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35106817

<400> 1832

atgcaggtgc cgggtgagga cggcatcatg ccgaaactgt tcggacggat c

51

<210> 1833

<211> 51

<212> DNA

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1834 is other entry)

<221> misc\_feature

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<223> Accession number cg35111750

<400> 1833

atattggatc tttccctggt tttttgtat ctagcagacc ttcattggtta t

51

<210> 1834

<211> 50

<212> DNA

<213> Homo sapiens

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<223> Accession number cg35111750

<400> 1834

atattggatc tttccctggt tttttgtatc tagcagacct tcattggttat

50

<210> 1835

<211> 51  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg35137271

<400> 1835  
agccaatggt gcacagtgat gatacgaatg tcaatctttg ctcggtcagt g 51

<210> 1836  
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<221> misc\_feature  
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<223> Accession number cg35137271

<400> 1836  
agccaatggt gcacagtgat gatacaaatg tcaatctttg ctcggtcagt g 51

<210> 1837  
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<223> 1 of 2 allelic variants (1838 is other entry)

<221> misc\_feature  
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<223> Accession number cg35137271

<400> 1837  
ttgctcggtc agtgaggatg tcgccctgac ccttctgct cccagaaag g 51

<210> 1838  
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<221> misc\_feature  
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<400> 1838  
ttgctcggtc agtgaggatg tcgccttgac ccttcctgct ccccagaaag g 51

<210> 1839  
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<212> DNA  
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<221> misc\_feature  
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<400> 1839  
tgaagtataa gaatattctg ctgctgttga gtggtatgta atgtatatgt c 51

<210> 1840  
<211> 51  
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<400> 1840  
tgaagtataa gaatattctg ctgcttttga gtggtatgta atgtatatgt c 51

<210> 1841  
<211> 45  
<212> DNA  
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1842 is other entry)

<221> misc\_feature  
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<223> Accession number cg35138283

<400> 1841  
gttttataca ttattgaaag tggaatatta gattctacca ctagt 45

<210> 1842  
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<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1841 is other entry)

<221> misc\_feature  
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<400> 1842  
gttttataca ttattgaaag tggaacatta gattctacca ctagt 45

<210> 1843  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1844 is other entry)

<221> misc\_feature  
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<223> Accession number cg35350458

<400> 1843  
ttctcgtcta gcagttattca gataccctt ctgctcagcc tgcttggcgt t 51

<210> 1844  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1843 is other entry)

<221> misc\_feature  
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<400> 1844  
ttctcgtcta gcagttattca gatactcctt ctgctcagcc tgcttggcgt t 51

<210> 1845  
<211> 51

<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1846 is other entry)

<221> misc\_feature  
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<223> Accession number cg35354409

<400> 1845  
ttttccggag ttatttaaaa aaaaaacaaa cagatgcctt ttaagggtta t 51

<210> 1846  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg35354409

<400> 1846  
ttttccggag ttatttaaaa aaaaacaaac agatgccttt taagggttat 50

<210> 1847  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1848 is other entry)

<221> misc\_feature  
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<223> Accession number cg35364749

<400> 1847  
cccatcacca acgccaccct ggaccgggtg agtgcctggg ctagccctgt c 51

<210> 1848  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1847 is other entry)

<221> misc\_feature  
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<223> Accession number cg35364749

<400> 1848  
cccatcacca acgccaccct ggaccaggtg agtgccctggg ctagccctgt c 51

<210> 1849  
<211> 51  
<212> DNA  
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<223> 1 of 2 allelic variants (1850 is other entry)

<221> misc\_feature  
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<223> Accession number cg35364849

<400> 1849  
gttgatgctt gatttaagag taagtgttat cgtgttcagt tttatatct c 51

<210> 1850  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1849 is other entry)

<221> misc\_feature  
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<223> Accession number cg35364849

<400> 1850  
gttgatgctt gatttaagag taagtattat cgtgttcagt tttatatct c 51

<210> 1851  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1852 is other entry)

<221> misc\_feature  
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<223> Accession number cg35817789

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ctcttagcaa ccaataattt ttttttcaat aattaagtac caatttcctg c

51

<210> 1852  
<211> 50  
<212> DNA  
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<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg35817789

<400> 1852  
ctcttagcaa ccaataattt tttttcaata attaagtacc aatttcctgc

50

<210> 1853  
<211> 51  
<212> DNA  
<213> Homo sapiens

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<223> 1 of 2 allelic variants (1854 is other entry)

<221> misc\_feature  
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<223> Accession number cg35817789

<400> 1853  
caatttcctg ctaatgggca ggccacacctt tattttctttt tttttccatt a

51

<210> 1854  
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<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1853 is other entry)

<221> misc\_feature  
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<223> Accession number cg35817789

<400> 1854

caatttctg ctaatgggca ggccccctt tatttctttt tttttccatt a

51

<210> 1855

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1856 is other entry)

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<223> Accession number cg35817789

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ctaatgggca ggcccacctt tatttctttt tttttccatt agaacgagca t

51

<210> 1856

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<212> DNA

<213> Homo sapiens

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51

<210> 1857

<211> 51

<212> DNA

<213> Homo sapiens

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<400> 1857

gaagagcact tgcagccgca tcaggtgaac atcaaactgc aaagccacct g

51

<210> 1858

<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1857 is other entry)

<221> misc\_feature  
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<400> 1858  
gaagagcact tgcagccgca tcaggcgaac atcaaactgc aaagccacct g

51

<210> 1859  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1860 is other entry)

<221> misc\_feature  
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<223> Accession number cg35927209

<400> 1859  
cccccttggt agtgggcgca cgaatcagtc ttcttcgcgg tccatggtga c

51

<210> 1860  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1859 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35927209

<400> 1860  
cccccttggt agtgggcgca cgaattagtc ttcttcgcgg tccatggtga c

51

<210> 1861  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 1 of 2 allelic variants (1862 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35927209

<400> 1861  
ccacgggatc accggcatcg cgcagaccga cgaagttaac ccctttaacg a 51

<210> 1862  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1861 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35927209

<400> 1862  
ccacgggatc accggcatcg cgcaggccga cgaagttaac ccctttaacg a 51

<210> 1863  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (1864 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35927209

<400> 1863  
gatcaccggc atcgcgcaga ccgacgaagt taaccccttt aacgaccgcg c 51

<210> 1864  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1863 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35927209

<400> 1864  
gatcaccggc atcgcgacaga ccgacaaaagt taaccctttt aacgaccgc c 51

<210> 1865  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1866 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35929317

<400> 1865  
gccgagcatg gtggcgggca cctgtagtcc cagccacctg ggaggctgag g 51

<210> 1866  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1865 is other entry)

<221> misc\_feature  
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<223> Accession number cg35929317

<400> 1866  
gccgagcatg gtggcgggca cctgtggtcc cagccacctg ggaggctgag g 51

<210> 1867  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1868 is other entry)

<221> misc\_feature  
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<223> Accession number cg35933276

<400> 1867  
atgagttcct gcgataaccc ggtagtctcg aaaatctggg ctccgtata c 51

<210> 1868  
<211> 51

<212> DNA  
<213> Homo sapiens  
  
<220>  
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<223> 2 of 2 allelic variants (1867 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35933276  
  
<400> 1868  
atgagttcct gcgataaccc ggtagcctcg aaaatctggg ctccggtata c 51  
  
<210> 1869  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
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<223> 1 of 2 allelic variants (1870 is other entry)  
  
<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35933276  
  
<400> 1869  
cctgcgataa cccggtagtc tcgaaaatct gggctccggt atacgacgag a 51  
  
<210> 1870  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg35933276  
  
<400> 1870  
cctgcgataa cccggtagtc tcgaagatct gggctccggt atacgacgag a 51  
  
<210> 1871  
<211> 51  
<212> DNA  
<213> Homo sapiens  
  
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<223> 1 of 2 allelic variants (1872 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1871

ccggtatacg acgagatagt ggatataccc atcttgctca tcgtcttaag g

51

<210> 1872

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (1871 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1872

ccggtatacg acgagatagt ggatacaccc atcttgctca tcgtcttaag g

51

<210> 1873

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (1874 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1873

taaggacgcc cttgccaaga gccttgtaaa cgttatggat agcagtttca g

51

<210> 1874

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1873 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1874  
taaggacgcc cttgccaaga gccttataaa cgttatggat agcagtttca g 51

<210> 1875  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1876 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35933276

<400> 1875  
taaacggttat ggatagcagt ttcaggggtca gtagacaccc acacctcgcg c 51

<210> 1876  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (1875 is other entry)

<221> misc\_feature  
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<400> 1876  
taaacggttat ggatagcagt ttcagagtca gtagacaccc acacctcgcg c 51

<210> 1877  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg35933276

<400> 1877  
ctgactcgaa gagcaaatac ggggtgacag ccgaagcacc ataaccatg a 51

<210> 1878  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1877 is other entry)

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<222> (0)...(0)

<223> Accession number cg35933276

<400> 1878

ctgactcgaa gagcaaatac gggttaacag ccgaagcacc ataaccatg a

51

<210> 1879

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1880 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35933276

<400> 1879

agagcaaata cgggttgaca gccgaagcac cataacccat gaggagggcg a

51

<210> 1880

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1879 is other entry)

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<223> Accession number cg35933276

<400> 1880

agagcaaata cgggttgaca gccgaggcac cataacccat gaggagggcg a

51

<210> 1881

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1882 is other entry)



<221> misc\_feature  
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<223> Accession number cg35933276

<400> 1881  
agcgatctcg gtcaggccga cccctcgat ggcactcgtc gttccggcga a 51

<210> 1882  
<211> 51  
<212> DNA  
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<220>  
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<223> Accession number cg35933276

<400> 1882  
agcgatctcg gtcaggccga ccccgcgat ggcactcgtc gttccggcga a 51

<210> 1883  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1884 is other entry)

<221> misc\_feature  
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<400> 1883  
ccctcgatgc gactcgtcgt tccggcgaag tactcatcaa tgagttcctg c 51

<210> 1884  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1883 is other entry)

<221> misc\_feature  
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<223> Accession number cg35933276

<400> 1884

ccctcgatgc gactcgtcgt tccggtgaag tactcatcaa tgagttcctg c

51

<210> 1885

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1886 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35980513

<400> 1885

aaaatgagcc gggcgtggtg acacacgcct gtagtcccag ctacttgga g

51

<210> 1886

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1885 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg35980513

<400> 1886

aaaatgagcc gggcgtggtg acacatgcct gtagtcccag ctacttgga g

51

<210> 1887

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (1888 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg36173201

<400> 1887

gcctccagaa ctgtgagaga ataaacgtcc gatgttttaa gccattcagt t

51

<210> 1888

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (1887 is other entry)

<221> misc\_feature  
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<223> Accession number cg36173201

<400> 1888  
gcctccagaa ctgtgagaga ataaatgtcc gatgttttaa gccattcagt t 51

<210> 1889  
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<212> DNA  
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<223> 1 of 2 allelic variants (1890 is other entry)

<221> misc\_feature  
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<223> Accession number cg36180692

<400> 1889  
gaggactgct tgagcccagg agttcaagac cagcctgggc aacacagtga g 51

<210> 1890  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1889 is other entry)

<221> misc\_feature  
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<223> Accession number cg36180692

<400> 1890  
gaggactgct tgagcccagg agttcgagac cagcctgggc aacacagtga g 51

<210> 1891  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1892 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36190410

<400> 1891  
acaggcgtga gccaccatgc ccagccttga atactgaatc taagtatttt t 51

<210> 1892  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1891 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36190410

<400> 1892  
acaggcgtga gccaccatgc ccagccttga atactgaatc taagtatttt t 51

<210> 1893  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1894 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36190410

<400> 1893  
ccagccttga atactgaatc taagtatttt ttgctagttt taaaataatt a 51

<210> 1894  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1893 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36190410

<400> 1894  
ccagccttga atactgaatc taagtatttt ttgctagttt taaaataatt a 51

<210> 1895  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1896 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36190410

<400> 1895  
tctagcatat gttaaagaa gtagattttt ttttaactc tccatttgat a 51

<210> 1896  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1895 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36190410

<400> 1896  
tctagcatat gttaaagaa gtagattttt ttttaactct ccatttgata 50

<210> 1897  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1898 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36504297

<400> 1897  
cgttttcttc agtgcttcat tttatactc aaattctgct gaagtgattt a 51

<210> 1898

<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1897 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36504297

<400> 1898  
cgttttcttc agtgcttcat tttatgcctc aaattctgct gaagtgattt a 51

<210> 1899  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1900 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36517624

<400> 1899  
cctcctcgtc gcggaacggg ctctcccga agcgctcctc cagctgccgg c 51

<210> 1900  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1899 is other entry)

<221> misc\_feature  
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<223> Accession number cg36517624

<400> 1900  
cctcctcgtc gcggaacggg ctctcgccga agcgctcctc cagctgccgg c 51

<210> 1901  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 1 of 2 allelic variants (1902 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36517624

<400> 1901  
ctgccggcga agcttctggg aactggccca gccaaactct tcaagctgct g 51

<210> 1902  
<211> 50  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1901 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36517624

<400> 1902  
ctgccggcga agcttctggg aactggccag ccaaactctt caagctgctg 50

<210> 1903  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1904 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36588981

<400> 1903  
aggagcacct caaggcctgt gacccgagca ccatgtcggg gtgtggctgc a 51

<210> 1904  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1903 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36588981

<400> 1904  
aggagcacct caaggcctgt gacccaagca ccatgtcggg gtgtggctgc a 51

<210> 1905  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1906 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36603177

<400> 1905  
tgagatcagg agttcgagac cagcccagcc aacatagtga aaccctgtct c 51

<210> 1906  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1905 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36603177

<400> 1906  
tgagatcagg agttcgagac cagcctagcc aacatagtga aaccctgtct c 51

<210> 1907  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1908 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36618790

<400> 1907



caggcacggt ggttcacgtc tgtaacccca gcactttggg aggctgagga a 51

<210> 1908

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1907 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg36618790

<400> 1908

caggcacggt ggttcacgtc tgtaatccca gcactttggg aggctgagga a 51

<210> 1909

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1910 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg36618790

<400> 1909

cagcactttg ggaggctgag gaaggcggat gacttgagcc caggagttag a 51

<210> 1910

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1909 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg36618790

<400> 1910

cagcactttg ggaggctgag gaaggcggat gacttgagcc caggagttag a 51

<210> 1911

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1912 is other entry)

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<222> (0)...(0)  
<223> Accession number cg36618790

<400> 1911  
ctttgggagg ctgaggaagg tggatgactt gagcccagga gtttgagacc a 51

<210> 1912  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1911 is other entry)

<221> misc\_feature  
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<223> Accession number cg36618790

<400> 1912  
ctttgggagg ctgaggaagg tggatcactt gagcccagga gtttgagacc a 51

<210> 1913  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1914 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36618790

<400> 1913  
gaaggtggat gacttgagcc caggagtttg agaccagcct gggcaacatg g 51

<210> 1914  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1913 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36618790

<400> 1914  
gaaggtggat gacttgagcc caggaatttg agaccagcct gggcaacatg g 51

<210> 1915  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg36623778

<400> 1915  
tgtgcctatc aaggttggtg tgcacggtg gaacgtgcc gtcacgtca c 51

<210> 1916  
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<223> Accession number cg36623778

<400> 1916  
tgtgcctatc aaggttggtg tgcacggtg gaacgtgcc gtcacgtca c 51

<210> 1917  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1918 is other entry)

<221> misc\_feature  
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<223> Accession number cg36733186

<400> 1917  
gctccacagg acaatgacct tggcccgtgg cccatcctct ctggcctcca t 51

<210> 1918  
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<212> DNA  
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<223> 2 of 2 allelic variants (1917 is other entry)

<221> misc\_feature  
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<223> Accession number cg36733186

<400> 1918  
gctccacagg acaatgacct tggccggtgg cccatcctct ctggcctcca t 51

<210> 1919  
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<223> 1 of 2 allelic variants (1920 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36753762

<400> 1919  
caggagtcca agaccagcct ggccaacatg atgaaaccct gtctctacta a 51

<210> 1920  
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<212> DNA  
<213> Homo sapiens

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<223> 2 of 2 allelic variants (1919 is other entry)

<221> misc\_feature  
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<223> Accession number cg36753762

<400> 1920  
caggagtcca agaccagcct ggccagcatg atgaaaccct gtctctacta a 51

<210> 1921  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1922 is other entry)

<221> misc\_feature  
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<223> Accession number cg36753762

<400> 1921  
ctactaaaaa tacacaaagt tagccaggcg tgggtggcacg tgccctgtaat c 51

<210> 1922  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1921 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36753762

<400> 1922  
ctactaaaaa tacacaaagt tagccgggcg tgggtggcacg tgccctgtaat c 51

<210> 1923  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (1924 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36999717

<400> 1923  
cctgcgcctt cggatacgat cagcgtctag aggcatttgg ggccgacggc a 51

<210> 1924  
<211> 51  
<212> DNA  
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<223> 2 of 2 allelic variants (1923 is other entry)

<221> misc\_feature

<222> (0)...(0)  
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<400> 1924  
cctgcgcctt cggatacgat cagcgcctag aggcatttgg ggccgacggc a 51

<210> 1925  
<211> 51  
<212> DNA  
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<223> 1 of 2 allelic variants (1926 is other entry)

<221> misc\_feature  
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<400> 1925  
gtctagaggc atttggggcc gacggcatgc ttagtgccga caacctcacc g 51

<210> 1926  
<211> 50  
<212> DNA  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg36999717

<400> 1926  
gtctagaggc atttggggcc gacggatgct tagtgccgac aacctcaccg 50

<210> 1927  
<211> 51  
<212> DNA  
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<223> 1 of 2 allelic variants (1928 is other entry)

<221> misc\_feature  
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<223> Accession number cg37003369

<400> 1927  
gtgagtttca gttgatttaa ggaataaaaa aagaccattt tgctaaacac t 51

<210> 1928  
<211> 50  
<212> DNA  
<213> Homo sapiens

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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg37003369

<400> 1928  
gtgagtttca gttgatttaa ggaataaaaa agaccatttt gctaaacact 50

<210> 1929  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (1930 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg37028403

<400> 1929  
caggtaaccc gcatattggt gctggtggag tgcccaacac ggcacttgga a 51

<210> 1930  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1929 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg37028403

<400> 1930

caggtaaccc gcatattgtt gctggcggag tgcccaacac ggcacttgga a

51

<210> 1931

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1932 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg37056126

<400> 1931

ctggggctca ggcctatga cccaacggcc attggtggcc tgtcctcatg g

51

<210> 1932

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1931 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg37056126

<400> 1932

ctggggctca ggcctatga cccaatggcc attggtggcc tgtcctcatg g

51

<210> 1933

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1934 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg37056126

<400> 1933

caaaccacaa tagcagttct ggggttatggg tttggtaaaa ccacctcagg g

51

<210> 1934

<211> 51

<212> DNA

<213> Homo sapiens



<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1933 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg37056126

<400> 1934  
caaaccacaa tagcagttct gggttttggg tttggtaaaa ccacctcagg g 51

<210> 1935  
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<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1936 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg37418902

<400> 1935  
atccacctca caaagaaatg caacacccat tagcggtcac tctcattctc c 51

<210> 1936  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (1935 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg37418902

<400> 1936  
atccacctca caaagaaatg caacatccat tagcggtcac tctcattctc c 51

<210> 1937  
<211> 51  
<212> DNA  
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<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1938 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg37418902

<400> 1937  
caaagaaatg caacacccat tagcggtcac tctcattctc cttgtccagc c 51

<210> 1938  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1937 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg37418902

<400> 1938  
caaagaaatg caacacccat tagcggtcac tctcattctc cttgtccagc c 51

<210> 1939  
<211> 51  
<212> DNA  
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<223> 1 of 2 allelic variants (1940 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38034239

<400> 1939  
ggcctggaac aggagagcgg gcgtagctcg ggcttctatg aagatcccag c 51

<210> 1940  
<211> 50  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1939 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg38034239

<400> 1940

ggcctggaac aggagagcgg gcgtactcgg gcttctatga agatcccagc

50

<210> 1941

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1942 is other entry)

<221> misc\_feature

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<223> Accession number cg38068769

<400> 1941

ttatgtcct catctttcta gattggttca gatgccctt ctaggaagcc t

51

<210> 1942

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1941 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38068769

<400> 1942

ttatgtcct catctttcta gattgattca gatgccctt ctaggaagcc t

51

<210> 1943

<211> 51

<212> DNA

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<220>

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<223> 1 of 2 allelic variants (1944 is other entry)

<221> misc\_feature

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<223> Accession number cg38068769

<400> 1943

tctagattgg ttcagatgcc ccttctagga agccttccca gattttcgcc c

51

<210> 1944

<211> 51  
<212> DNA  
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<223> 2 of 2 allelic variants (1943 is other entry)

<221> misc\_feature  
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<223> Accession number cg38068769

<400> 1944  
tctagattgg ttcagatgcc ccttccagga agccttccca gattttcgcc c 51

<210> 1945  
<211> 51  
<212> DNA  
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<223> 1 of 2 allelic variants (1946 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38070669

<400> 1945  
actggtatgc cactgaaaaa aaaaaacaaa aaaacaaaac ccaaagccaa a 51

<210> 1946  
<211> 50  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (1945 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38070669

<400> 1946  
actggtatgc cactgaaaaa aaaaacaaaa aaacaaaacc caaagccaaa 50

<210> 1947  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1948 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38206730

<400> 1947

agggtgtgccca catgttcatt ttcgggtcaa ggcgtacacg tgcaggtgtg t

51

<210> 1948

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1947 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38206730

<400> 1948

agggtgtgccca catgttcatt ttcgggtcaa ggcgtacacg tgcaggtgtg t

51

<210> 1949

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (1950 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38206730

<400> 1949

gttcatttttc ggttcaaggc gtacacgtgc aggtgtgtta cgtgttcatt t

51

<210> 1950

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (1949 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38206730

<400> 1950  
gttcattttc ggttcaaggc gtacatgtgc aggtgtgtta cgtgttcatt t 51

<210> 1951  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (1952 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38276118

<400> 1951  
ttttgaaatt agccaaaaaa aaaaatcaaa ccttaaacad tgttcaattc 50

<210> 1952  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1951 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38276118

<400> 1952  
ttttgaaatt agccaaaaaa aaaaatcaa accttaaca ttgttcaatt c 51

<210> 1953  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1954 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38277495

<400> 1953

cagcaccttg ggaggctgag gtgggcggat cacctgaggt tgggagttcg a

51

<210> 1954

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1953 is other entry)

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<222> (0)...(0)

<223> Accession number cg38277495

<400> 1954

cagcaccttg ggaggctgag gtgggtggat cacctgaggt tgggagttcg a

51

<210> 1955

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1956 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38278604

<400> 1955

caggaatgtg atagaaagtg gctgggaaga gggagctgag gctggtgggt c

51

<210> 1956

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1955 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38278604

<400> 1956

caggaatgtg atagaaagtg gctggcaaga gggagctgag gctggtgggt c

51

<210> 1957  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1958 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38279706

<400> 1957  
tgcagctcca tggctcaaca aggtgcggat gcctgctgga cctggctgct t 51

<210> 1958  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1957 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38279706

<400> 1958  
tgcagctcca tggctcaaca aggtgtggat gcctgctgga cctggctgct t 51

<210> 1959  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1960 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38318472

<400> 1959  
ccacgtgtca tgactgtctg tccttctcca aggcagcatt cagacacccc g 51

<210> 1960  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>



<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1959 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38318472

<400> 1960  
ccacgtgtca tgactgtctg tccttttcca aggcagcatt cagacacccc g 51

<210> 1961  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1962 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38323872

<400> 1961  
cgccccgctc ggccaccaaaa aatgctggga ccacaggctg taatttattt t 51

<210> 1962  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1961 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38323872

<400> 1962  
cgccccgctc ggccaccaaaa aatgccggga ccacaggctg taatttattt t 51

<210> 1963  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1964 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg38323872

<400> 1963

gcctcggcca ccaaaaatgc tgggaccaca ggctgtaatt tatttttttc a

51

<210> 1964

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1963 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38323872

<400> 1964

gcctcggcca ccaaaaatgc tgggatcaca ggctgtaatt tatttttttc a

51

<210> 1965

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (1966 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38323872

<400> 1965

cctcggccac caaaaatgct gggaccacag gctgtaattt atttttttca t

51

<210> 1966

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (1965 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38323872

<400> 1966

cctcggccac caaaaatgct gggactacag gctgtaattt atttttttca t

51

<210> 1967

<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1968 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38326936

<400> 1967  
tgcgcggcct ggcacgctg ctggctaaga acaaccggct cggcgggccc a 51

<210> 1968  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (1967 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38326936

<400> 1968  
tgcgcggcct ggcacgctg ctggccaaga acaaccggct cggcgggccc a 51

<210> 1969  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (1970 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38338993

<400> 1969  
ctgtagccta agcaacagag caagatgccg tctctgaaaa ggaaagaaaa c 51

<210> 1970  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<210> 1977  
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<210> 1978  
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aggctgcgga ctttctatct gaatacgcca ccgaagatat ggaccttgcc g 51

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aggctgcgga ctttctatct gaatatgcca ccgaagatat ggaccttgcc g 51

<210> 2029  
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<210> 2030  
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<210> 2031  
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<210> 2032  
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<400> 2032  
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<210> 2033  
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<212> DNA  
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<221> misc\_feature  
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actggtcccg cgtggagcga tacttctttg aggactgact gctgggcagg g 51

<210> 2034  
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<212> DNA  
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<221> misc\_feature  
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<210> 2035  
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<221> misc\_feature  
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<400> 2035  
actgctgggc aggggtgagc gatgcgatga tggtgagaat ttcgcctatt c 51

<210> 2036  
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<221> misc\_feature  
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<210> 2037  
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<221> misc\_feature

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51

<210> 2038

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2037 is other entry)

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<210> 2039

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2040 is other entry)

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<222> (0)...(0)

<223> Accession number cg38403345

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<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2039 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38403345



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<210> 2041  
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<221> misc\_feature  
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catatcacca tccgtagtgc cgcgacgaag atcccagatg gccgttcttg g 51

<210> 2042  
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<221> misc\_feature  
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<210> 2043  
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<221> misc\_feature  
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tcttggaacct gtatatgacg tatggtcttg tcgggtagct tactggcgca g 51

<210> 2044  
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<223> 2 of 2 allelic variants (2043 is other entry)

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51

<210> 2045

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<223> 1 of 2 allelic variants (2046 is other entry)

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<222> (0)...(0)

<223> Accession number cg38403345

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51

<210> 2046

<211> 51

<212> DNA

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<210> 2047

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<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2048 is other entry)

<221> misc\_feature  
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<400> 2047  
gctgggagtt tctcgcgttc caccagcccc aaggacacca gcacgttgag g 51

<210> 2048  
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gctgggagtt tctcgcgttc caccaacccc aaggacacca gcacgttgag g 51

<210> 2049  
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<221> misc\_feature  
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<400> 2049  
gttcaccag cccaaggac accagcacgt tgaggggctc ccgaatcgtg t 51

<210> 2050  
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gttcaccag cccaaggac accagtacgt tgaggggctc ccgaatcgtg t

51

<210> 2051

<211> 51

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<222> (0)...(0)

<223> Accession number cg38403377

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aaatcttctt gacgatgacg tgcccttgtc tgagcgatcc ctgcttcgtc g

51

<210> 2052

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<212> DNA

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<223> Accession number cg38403377

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51

<210> 2053

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51

<210> 2054

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<221> misc\_feature  
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<210> 2055  
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<210> 2056  
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<221> misc\_feature  
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<210> 2057  
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<221> misc\_feature  
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cctctgcgac atatcgctgg gccgatgagg catcgacgat ctccccgcgg t 51

<210> 2058  
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<221> misc\_feature  
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<400> 2058  
cctctgcgac atatcgctgg gccgacgagg catcgacgat ctccccgcgg t 51

<210> 2059  
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<223> 1 of 2 allelic variants (2060 is other entry)

<221> misc\_feature  
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<223> Accession number cg38420254

<400> 2059  
tccaggaaag gacaatgtcc tgcgagaaaa tcaggaggcc tccacttcct g 51

<210> 2060  
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<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg38420254

<400> 2060

tccaggaaag gacaatgtcc tgcgaaaaat caggaggcct ccacttcctg

50

<210> 2061

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2062 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38420254

<400> 2061

cagtcaataa ttgtctttgt ggatgtgata attttggaga tacacttctg g

51

<210> 2062

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2061 is other entry)

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<222> (0)...(0)

<223> Accession number cg38420254

<400> 2062

cagtcaataa ttgtctttgt ggatgcgata attttggaga tacacttctg g

51

<210> 2063

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2064 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38421034

<400> 2063

ggtgactctg agcaagttct ggagccgcac gcacaagggg ctctgaaca g

51

<210> 2064

<211> 51  
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<221> misc\_feature  
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<400> 2064  
ggtgactctg agcaagttct ggagctgcac gcacaagggg ctctgaaca g 51

<210> 2065  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg38421040

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ttggcccgtg tggtcaccct gtgttcattct ctctcccagc catggcctct c 51

<210> 2066  
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<223> 2 of 2 allelic variants (2065 is other entry)

<221> misc\_feature  
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<223> Accession number cg38421040

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ttggcccgtg tggtcaccct gtgtttattct ctctcccagc catggcctct c 51

<210> 2067  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature



<222> (26)...(0)  
<223> 1 of 2 allelic variants (2068 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38433776

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aggcgtcgta gtgggccacg atgacgatgg tgggaaggtc ctctccgcc a 51

<210> 2068  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2067 is other entry)

<221> misc\_feature  
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<223> Accession number cg38433776

<400> 2068  
aggcgtcgta gtgggccacg atgacaatgg tgggaaggtc ctctccgcc a 51

<210> 2069  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2070 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38438371

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acctcgctga ttcgtgcaga ttgagctcag tgtgtctggg actgagctaa a 51

<210> 2070  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2069 is other entry)

<221> misc\_feature  
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<223> Accession number cg38438371

<400> 2070  
acctcgctga ttcgtgcaga ttgagttcag tgtgtctggg actgagctaa a 51

<210> 2071  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2072 is other entry)

<221> misc\_feature  
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<223> Accession number cg38438371

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ctgggactga gctaaacagt gagacgtttg gaccgtcttt gatgtacaga g 51

<210> 2072  
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<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2071 is other entry)

<221> misc\_feature  
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<223> Accession number cg38438371

<400> 2072  
ctgggactga gctaaacagt gagacatttg gaccgtcttt gatgtacaga g 51

<210> 2073  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg38438475

<400> 2073

ggaagagggg aaggaaaagg cagcctaagg gaaggcgctg gcctgaatca

50

<210> 2074

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38438475

<400> 2074

ggaagagggg aaggaaaagg cagccgtaag ggaaggcgct ggctgaatc a

51

<210> 2075

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2076 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38438944

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51

<210> 2076

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2075 is other entry)

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<223> Accession number cg38438944

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51

<210> 2077

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<212> DNA

<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2078 is other entry)

<221> misc\_feature  
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<223> Accession number cg38439545

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cctggcggcc agtaccagag cacagtccgg agtcttccgg cgggatgcat g 51

<210> 2078  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<210> 2079  
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<220>  
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<223> 1 of 2 allelic variants (2080 is other entry)

<221> misc\_feature  
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<223> Accession number cg38444370

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gcatcgtttc gacgatgaac cccatcctgg gagcagatat gacgacgtac c 51

<210> 2080  
<211> 51  
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (2079 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38444370

<400> 2080  
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<210> 2081  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg38444370

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agttcacctg ggaccaggtc gaccttgcta ctgtcgaga caccggtcgg g 51

<210> 2082  
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<220>  
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<221> misc\_feature  
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<400> 2082  
agttcacctg ggaccaggtc gacctcgcta ctgtcgaga caccggtcgg g 51

<210> 2083  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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tcgaggactt cgttttatcg gaggattcgt cgcgcaaccg atcaatctca g 51

<210> 2084  
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<212> DNA  
<213> Homo sapiens

<220>  
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<400> 2084  
tcgaggactt cgttttatcg gaggactcgt cgcgcaaccg atcaatctca g 51

<210> 2085  
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<221> misc\_feature  
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caatctcagt agcgaagtcc tcgatggtgt tgtagttcaa gttaaagctg g 51

<210> 2086  
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<221> misc\_feature  
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<210> 2087  
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<221> misc\_feature  
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tagcgaagtc ctcgatggtg ttgtagttca agtaaagct ggcaaacctc a 51

<210> 2088  
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tagcgaagtc ctcgatggtg ttgtacttca agtaaagct ggcaaacctc a 51

<210> 2089  
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<220>  
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<221> misc\_feature  
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<400> 2089  
ctggcaaacc tcaggtaagc gatggaatca agttcacgca gtggcccca g 51

<210> 2090  
<211> 51  
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<221> misc\_feature

<222> (0)...(0)  
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<400> 2090  
ctggcaaacc tcaggtaagc gatgggatca agttcacgca gtggcccca g 51

<210> 2091  
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<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2092 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38446357

<400> 2091  
acctcaggta agcgatggaa tcaagttcac gcagtggccc caagatcgcc a 51

<210> 2092  
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<220>  
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<221> misc\_feature  
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<400> 2092  
acctcaggta agcgatggaa tcaagctcac gcagtggccc caagatcgcc a 51

<210> 2093  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg38446612

<400> 2093  
gcgtagagt cgtcttgccg ggcgcgttgc gaccactag accgaccttg t 51



<210> 2094  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg38446612

<400> 2094  
gcgttagagt cgtcttgccg gcgccattgc gaccactag accgaccttg t 51

<210> 2095  
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<220>  
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<221> misc\_feature  
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gcgccgttgc gaccactag accgaccttg tccccagtag ctacctggaa a 51

<210> 2096  
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<221> misc\_feature  
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<223> Accession number cg38446612

<400> 2096  
gcgccgttgc gaccactag accgatcttg tccccagtag ctacctggaa a 51

<210> 2097  
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<220>

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<223> 1 of 2 allelic variants (2098 is other entry)

<221> misc\_feature  
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<400> 2097  
tgcgaccac tagaccgacc ttgtcccag tagctacctg gaaactcacc g 51

<210> 2098  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<400> 2098  
tgcgaccac tagaccgacc ttgtctccag tagctacctg gaaactcacc g 51

<210> 2099  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2100 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38446677

<400> 2099  
gatcggcgt tcccgggttcg atagggggcg ttatagtcac gatcaccacc t 51

<210> 2100  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2099 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg38446677

<400> 2100

gatcggcggg tccccggttcg ataggtggcg ttatagtcac gatcaccacc t

51

<210> 2101

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2102 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38446677

<400> 2101

atcatgggtg acgacgacga ggggtggtcc cgcgccgggc gtcgccgaaa g

51

<210> 2102

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2101 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38446677

<400> 2102

atcatgggtg acgacgacga ggggtggtccc cgccccgggc tcgccgaaag

50

<210> 2103

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2104 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38453366

<400> 2103  
tcttcgagtt tttgttcaag tctgggtctt ctgactgatt ttccaatgtc c 51

<210> 2104  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2103 is other entry)

<221> misc\_feature  
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<223> Accession number cg38453366

<400> 2104  
tcttcgagtt tttgttcaag tctgggtctt ctgactgatt ttccaatgtc c 51

<210> 2105  
<211> 51  
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<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38453366

<400> 2105  
ctgggtcttc tgactgattt tccaatgtcc aaggtgctga accgaatgca a 51

<210> 2106  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2105 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38453366

<400> 2106  
ctgggtcttc tgactgattt tccaaagtcc aaggtgctga accgaatgca a 51

<210> 2107  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2108 is other entry)

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<223> Accession number cg38453366

<400> 2107

tctgactgat tttccaatgt ccaaggtgct gaaccgaatg caatcaccat t

51

<210> 2108

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2107 is other entry)

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<222> (0)...(0)

<223> Accession number cg38453366

<400> 2108

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51

<210> 2109

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2110 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38453366

<400> 2109

ctgattttcc aatgtccaag gtgctgaacc gaatgcaatc accattcaat g

51

<210> 2110

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2109 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38453366

<400> 2110  
ctgattttcc aatgtccaag gtgcttaacc gaatgcaatc accattcaat g 51

<210> 2111  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2112 is other entry)

<221> misc\_feature  
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<223> Accession number cg38453366

<400> 2111  
ttttccaatg tccaaggtgc tgaaccgaat gcaatcacca ttcaatgaca g 51

<210> 2112  
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<220>  
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<223> 2 of 2 allelic variants (2111 is other entry)

<221> misc\_feature  
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<400> 2112  
ttttccaatg tccaaggtgc tgaactgaat gcaatcacca ttcaatgaca g 51

<210> 2113  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2114 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 2113

aatgtccaag gtgctgaacc gaatgcaatc accattcaat gacagctcaa c 51

<210> 2114

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2113 is other entry)

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<223> Accession number cg38453366

<400> 2114

aatgtccaag gtgctgaacc gaatgtaatc accattcaat gacagctcaa c 51

<210> 2115

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2116 is other entry)

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<400> 2115

ctgaaccgaa tgcaatcacc attcaatgac agtcaactt ccaaatttct t 51

<210> 2116

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2115 is other entry)

<221> misc\_feature

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<223> Accession number cg38453366

<400> 2116

ctgaaccgaa tgcaatcacc attcactgac agtcaactt ccaaatttct t 51

<210> 2117

<211> 50

<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2118 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38453366

<400> 2117  
accgaatgca atcaccattc aatgacagct caacttccaa atttctttga 50

<210> 2118  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (2117 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 2118  
accgaatgca atcaccattc aatgaacagc tcaacttcca aatttctttg a 51

<210> 2119  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2120 is other entry)

<221> misc\_feature  
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<400> 2119  
caatcaccat tcaatgacag ctcaacttcc aaatttcttt gaatttcttt t 51

<210> 2120  
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<213> Homo, sapiens

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<221> misc\_feature  
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<221> misc\_feature  
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<400> 2120  
caatcacat tcaatgacag ctcaatttcc aaatttcttt gaatttcttt t 51

<210> 2121  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2122 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38453366

<400> 2121  
aatttctttt aacagaacaa tccaatatga aaatcagaat ctcttctgac g 51

<210> 2122  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2121 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 2122  
aatttctttt aacagaacaa tccaacatga aaatcagaat ctcttctgac g 51

<210> 2123  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2124 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg38453366

<400> 2123

ttaacagaac aatccaatat gaaaatcaga atctcttctg acggtgggag a

51

<210> 2124

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2123 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38453366

<400> 2124

ttaacagaac aatccaatat gaaaaccaga atctcttctg acggtgggag a

51

<210> 2125

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2126 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38606941

<400> 2125

tacagatata tacaagattc ccacctgtat gcaattctct gggtcattctg t

51

<210> 2126

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2125 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38606941

<400> 2126

tacagatata tacaagattc ccaccgtat gcaattctct gggtcattctg t

51

<210> 2127

<211> 41  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (16)...(0)  
<223> 1 of 2 allelic variants (2128 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38624864

<400> 2127  
accggtccca gacagtggga tgccaggacc ccttttgcag g

41

<210> 2128  
<211> 41  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (16)...(0)  
<223> 2 of 2 allelic variants (2127 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38624864

<400> 2128  
accggtccca gacaggggga tgccaggacc ccttttgcag g

41

<210> 2129  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2130 is other entry)

<221> misc\_feature  
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<223> Accession number cg38628815

<400> 2129  
gttgacagc ctctccaact cccagcctcc aggaatcctc cagcctcagc c

51

<210> 2130  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2129 is other entry)

<221> misc\_feature  
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<400> 2130  
gttgacacagg ctctccaact ccagtcctcc aggaatcctc cagcctcagc c 51

<210> 2131  
<211> 51  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg38683973

<400> 2131  
ctttcaaagt ctttaataac agggacgagc aaaataaatt agataaagcc`c 51

<210> 2132  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2131 is other entry)

<221> misc\_feature  
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<223> Accession number cg38683973

<400> 2132  
ctttcaaagt ctttaataac agggatgagc aaaataaatt agataaagcc c 51

<210> 2133  
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<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg38683973

<400> 2133  
agagatcgtg ctaaatacca gcttccagca gtggctatct gtcagtctag c 51

<210> 2134  
<211> 51  
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<223> 2 of 2 allelic variants (2133 is other entry)

<221> misc\_feature  
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<400> 2134  
agagatcgtg ctaaatacca gcttctagca gtggctatct gtcagtctag c 51

<210> 2135  
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<212> DNA  
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<223> 1 of 2 allelic variants (2136 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38691768

<400> 2135  
ctcccaaagt gctgggatta caggcatgag ccaactgcgcc cagcctcaaa c 51

<210> 2136  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (2135 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38691768

<400> 2136  
ctcccaaagt gctgggatta caggcgtgag ccaactgcgcc cagcctcaaa c 51

<210> 2137  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2138 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38753049

<400> 2137  
gcagccttga cctcctgggc tcaagcgatc cttctgcctc agcctcccaa g 51

<210> 2138  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2137 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38753049

<400> 2138  
gcagccttga cctcctgggc tcaagtgatc cttctgcctc agcctcccaa g 51

<210> 2139  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2140 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38863525

<400> 2139  
gggatcacca agatggaaga gtcggcagag tacgaggcag cgcggcataa a 51

<210> 2140  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2139 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38863525

<400> 2140

gggatcacca agatggaaga gtcggtagag tacgaggcag cgcggcataa a

51

<210> 2141

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2142 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38864699

<400> 2141

gctgccgagc ctgggtctga gcaggcgggg atgaggacca ggtgctgagg c

51

<210> 2142

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2141 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38864699

<400> 2142

gctgccgagc ctgggtctga gcagggtggg atgaggacca ggtgctgagg c

51

<210> 2143

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2144 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38866989

<400> 2143  
acagaacccat cctggcagat ggcaacggct gtagagaaga cccgcaggcc c 51

<210> 2144  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2143 is other entry)

<221> misc\_feature  
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<223> Accession number cg38866989

<400> 2144  
acagaacccat cctggcagat ggcaatggct gtagagaaga cccgcaggcc c 51

<210> 2145  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2146 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38868761

<400> 2145  
tctggggtag gggctgctcc cccaagtccc tgggggactg tctgggacat c 51

<210> 2146  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2145 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38868761

<400> 2146  
tctggggtag gggctgctcc cccaaatccc tgggggactg tctgggacat c 51

<210> 2147  
<211> 51  
<212> DNA



<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2148 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38868761

<400> 2147

tctgggacat ccaggccctg tcttcttgct ttaaccactc acaacagaga a

51

<210> 2148

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2147 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38868761

<400> 2148

tctgggacat ccaggccctg tcttcgtgct ttaaccactc acaacagaga a

51

<210> 2149

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2150 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38868761

<400> 2149

aagaaggccc cacacttctc ccatccggcc tccacgtaaa cgcgt

45

<210> 2150

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2149 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38868761

<400> 2150  
aagaaggccc cacacttctc ccatctggcc tccacgtaaa cgcgt 45

<210> 2151  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2152 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38879618

<400> 2151  
gctgagagca ggagtagaag gtctgcaagc agcatttgag aagtcataga a 51

<210> 2152  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2151 is other entry)

<221> misc\_feature  
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<223> Accession number cg38879618

<400> 2152  
gctgagagca ggagtagaag gtctgtaagc agcatttgag aagtcataga a 51

<210> 2153  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2154 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38879658

<400> 2153

gatcagaata actccagagc actgcggtgt ttctgactgg ctgaaattga t

51

<210> 2154

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2153 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38879658

<400> 2154

gatcagaata actccagagc actgctgtgt ttctgactgg ctgaaattga t

51

<210> 2155

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2156 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38880100

<400> 2155

tcagttacgc gattccgtga tcgcaaagct tgaaagactc gagcctggac g

51

<210> 2156

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2155 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38880100

<400> 2156

tcagttacgc gattccgtga tcgcagagct tgaaagactc gagcctggac g

51

<210> 2157

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2158 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38880100

<400> 2157  
cgagcctgga cgccagggtga ttgtgagctc gttcaaccat gtgctgttat c 51

<210> 2158  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2157 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38880100

<400> 2158  
cgagcctgga cgccagggtga ttgtgcgctc gttcaaccat gtgctgttat c 51

<210> 2159  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2160 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38884905

<400> 2159  
caaagcaact gtgaccgaaa accaactgca agattctcaa gagccctgaa g 51

<210> 2160  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2159 is other entry)

<221> misc\_feature  
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<223> Accession number cg38884905

<400> 2160  
caaagcaact gtgaccgaaa accaaatgca agattctcaa gagccctgaa g 51

<210> 2161  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2162 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38884905

<400> 2161  
aatcatccaa gaacacacta agcccgccaa gggcccaccc tgaccatgtg g 51

<210> 2162  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2161 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38884905

<400> 2162  
aatcatccaa gaacacacta agccccaag ggcccaccct gaccatgtgg 50

<210> 2163  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2164 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg38890535

<400> 2163

cacacgcgtt ggcggagaaa cacttcgccc acagtgtagg gcctcgcttg g

51

<210> 2164

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2163 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38890535

<400> 2164

cacacgcgtt ggcggagaaa cactttgccc acagtgtagg gcctcgcttg g

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<210> 2165

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2166 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38892055

<400> 2165

ccgagaggct ggcgaggggtg tgcagcacgg cgcagtgtgg caggggtccca g

51

<210> 2166

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2165 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38892055

<400> 2166

ccgagaggct ggcgaggggtg tgcagtacgg cgcagtgtgg caggggtccca g

51

<210> 2167

<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2168 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38892055

<400> 2167  
gatgaactgt cttcccacgg ccaccaggac gccactcgcc gcctgctgcc a

51

<210> 2168  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2167 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38892055

<400> 2168  
gatgaactgt cttcccacgg ccaccgggac gccactcgcc gcctgctgcc a

51

<210> 2169  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2170 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38892771

<400> 2169  
tctcttctgg tttcccaggc gtgtctgcct ctctgaaggt ttagctctcc c

51

<210> 2170  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 2 of 2 allelic variants (2169 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38892771

<400> 2170  
tctcttcttg tttcccaggc gtgtccgcct ctctgaaggt ttagctctcc c 51

<210> 2171  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2172 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38898718

<400> 2171  
gacgaccgtg cccgtacaag ccgaagcaac cgtcccaaaa agtacagaag g 51

<210> 2172  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2171 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38898718

<400> 2172  
gacgaccgtg cccgtacaag ccgaaacaac cgtcccaaaa agtacagaag g 51

<210> 2173  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2174 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38898718



<400> 2173  
ccaggacgcc ctttcctcaa cccttctggc aagactccgg atgctggctc t 51

<210> 2174  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2173 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38898718

<400> 2174  
ccaggacgcc ctttcctcaa cccttttggc aagactccgg atgctggctc t 51

<210> 2175  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2176 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38898718

<400> 2175  
tttcctcaac ccttctggca agactccgga tgctggctct tctcagtgg c 51

<210> 2176  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2175 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38898718

<400> 2176  
tttcctcaac ccttctggca agactacgga tgctggctct tctcagtgg c 51

<210> 2177  
<211> 51

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2178 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38898718

<400> 2177  
ccttctggca agactccgga tgctggctct tcctcagtg cagccctta a

51

<210> 2178  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2177 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38898718

<400> 2178  
ccttctggca agactccgga tgctgactct tcctcagtg cagccctta a

51

<210> 2179  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2180 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38898734

<400> 2179  
acatggtgtc accttgaata ggaatctcag gcaatcgaga cagagagagc c

51

<210> 2180  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)

<223> 2 of 2 allelic variants (2179 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38898734

<400> 2180

acatggtgtc accttgaata ggaatttcag gcaatcgaga cagagagagc c

51

<210> 2181

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2182 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38899892

<400> 2181

gccaagatgc caacgagcag ggccaagatt tggggaagag ggaccaccat g

51

<210> 2182

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2181 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38899892

<400> 2182

gccaagatgc caacgagcag ggccaggatt tggggaagag ggaccaccat g

51

<210> 2183

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2184 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38902436

<400> 2183  
tgaccgggcc tctgtggagg atgacagacg tagtggctgc cttcctagcc c 51

<210> 2184  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2183 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38902436

<400> 2184  
tgaccgggcc tctgtggagg atgacggacg tagtggctgc cttcctagcc c 51

<210> 2185  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2186 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38907673

<400> 2185  
gagcgcacag agtgctgtcg ggggcatga atggccagaa tttcagagct g 51

<210> 2186  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2185 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg38907673

<400> 2186  
gagcgcacag agtgctgtcg ggggcatga atggccagaa tttcagagct g 51

<210> 2187  
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<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2188 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38907673

<400> 2187

gagtagccgc aggtgcaagg acacagaaca gggtgaggaa agagtttggt t

51

<210> 2188

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2187 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38907673

<400> 2188

gagtagccgc aggtgcaagg acacataaca gggtgaggaa agagtttggt t

51

<210> 2189

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2190 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg38909281

<400> 2189

aactccttag ttgagtaccc tgtttgagcgt ccaatgggtg ggtgtcagaa t

51

<210> 2190

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

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<210> 2191  
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aagaagggggg ttgttttcag gaaagcactg ttagcatctt tgtttcaaag t 51

<210> 2192  
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51

<210> 2194

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<400> 2194

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<210> 2195

<211> 51

<212> DNA

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<222> (0)...(0)

<223> Accession number cg38916043

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51

<210> 2196

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2195 is other entry)

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<223> Accession number cg38916043

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cagaggatgg atatggcagc cgcagtacgg gcacatgtgg ttcgctgagc a

51

<210> 2197

<211> 51

<212> DNA

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agcatggcgc cggagtgcgc tgcgatggtg atgaggtgac gcgggggggat t 51

<210> 2198  
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<210> 2199  
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<210> 2200  
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<210> 2201  
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<221> misc\_feature  
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<210> 2202  
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<210> 2203  
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<221> misc\_feature  
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<210> 2204

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2203 is other entry)

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<400> 2204

aatggcgaat ggcgaaatgg tgctgcgcgg tggattatcc gttggtgtgc c

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<210> 2205

<211> 51

<212> DNA

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cacggcgtca tgcttgctca gctcaaccgc ggtgaaacag tcagaggatg g

51

<210> 2206

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<212> DNA

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<223> 2 of 2 allelic variants (2205 is other entry)

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51

<210> 2207

<211> 51

<212> DNA

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<400> 2207  
gcgtcatgct tgctcagctc aaccgcggtg aaacagtcag aggatggata t 51

<210> 2208  
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<400> 2208  
gcgtcatgct tgctcagctc aaccgtggtg aaacagtcag aggatggata t 51

<210> 2209  
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<223> 1 of 2 allelic variants (2210 is other entry)

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<400> 2209  
acgatgaggg ccataccga gaagacaacg gccaccactc gcagaccacc t 51

<210> 2210  
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<222> (0)...(0)  
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<210> 2211  
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<221> misc\_feature  
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<400> 2211  
gggaggatcg cggccactga ccacgccagt accggcaggg tcaggatcag c 51

<210> 2212  
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<221> misc\_feature  
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<210> 2213  
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<221> misc\_feature  
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<400> 2213  
taccgggaca gttacgagtc catgtccgag ccgccattg ctcacctttt g 51

<210> 2214  
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<221> misc\_feature  
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51

<210> 2215  
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51

<210> 2216  
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<210> 2217  
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cgaggcggtg aggcacccc gcgcagccca catcatcatc gtggagacga t

51

<210> 2218  
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<221> misc\_feature  
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<221> misc\_feature  
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<210> 2219  
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51

<210> 2220  
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<400> 2220  
atggcaagag ctggccaccc accctcccc ttccttccca aaggctgtgt 50

<210> 2221  
<211> 51  
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<400> 2221  
gagctggcca cccaccccct ccccttcctt cccaaaggct gtgttttgtc t 51

<210> 2222  
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<221> misc\_feature  
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<400> 2222  
gagctggcca cccaccccct ccccttcctt ccaaaggctg tggtttgtct 50

<210> 2223  
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<212> DNA  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39331132

<400> 2223  
tgtgacatgc tgttttaatt tcagtgcacct cttggaaggc actgtcccca a 51

<210> 2224  
<211> 51  
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<220>  
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<223> 2 of 2 allelic variants (2223 is other entry)

<221> misc\_feature  
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<223> Accession number cg39331132

<400> 2224  
tgtgacatgc tgttttaatt tcagtaacct cttggaaggc actgtcccca a 51

<210> 2225  
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<210> 2226  
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<223> 2 of 2 allelic variants (2225 is other entry)

<221> misc\_feature

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<223> Accession number cg39357997

<400> 2226

cctctaggaa cccaaccttc tgcgtccata cacgcgctcg cgcgcacacg c

51

<210> 2227

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2228 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39357997

<400> 2227

gcacacacac acacacacac acacacagca agcaagccat ctccggtcac a

51

<210> 2228

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2227 is other entry)

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<222> (0)...(0)

<223> Accession number cg39357997

<400> 2228

gcacacacac acacacacac acacaagcaa gcaagccatc tccggtcaca

50

<210> 2229

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2230 is other entry)

<221> misc\_feature  
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<223> Accession number cg39386977

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tggttttttac accagcagtc aaaaagagtt acttttgata ttgcatgtgt c 51

<210> 2230  
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<221> misc\_feature  
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<223> Accession number cg39386977

<400> 2230  
tggttttttac accagcagtc aaaaacagtt acttttgata ttgcatgtgt c 51

<210> 2231  
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<220>  
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<223> 1 of 2 allelic variants (2232 is other entry)

<221> misc\_feature  
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<223> Accession number cg39413590

<400> 2231  
aaaggaatat cctctcacca gagacacgcg gcggccaggc agggccggag c 51

<210> 2232  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg39413590

<400> 2232

aaaggaatat cctctcacca gagaccgcgg cggccaggca gggccggagc

50

<210> 2233

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2234 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39413590

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gagctcttgg agccacacct gcgtgtgcac atgtgtcacc ccaactgctgg g

51

<210> 2234

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2233 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39413590

<400> 2234

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<210> 2235

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<212> DNA

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<400> 2235

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51

<210> 2236

<211> 50  
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<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg39434475

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gccctgctgt ggatggaatc cggagacccc agctccctga gcagcccctc

50

<210> 2237  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2238 is other entry)

<221> misc\_feature  
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<223> Accession number cg39457156

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cagcgtaaag tggcataccc ggaaggaaac acagcagctc ttggatatga t

51

<210> 2238  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2237 is other entry)

<221> misc\_feature  
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<223> Accession number cg39457156

<400> 2238  
cagcgtaaag tggcataccc ggaagaaaac acagcagctc ttggatatga t

51

<210> 2239  
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<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2240 is other entry)

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actatggtgc catggtcgtc gatgcagcgc tgttcctgcc acagtcacga c

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<210> 2240

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<223> 2 of 2 allelic variants (2239 is other entry)

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<223> Accession number cg39457156

<400> 2240

actatggtgc catggtcgtc gatgctgcgc tgttcctgcc acagtcacga c

51

<210> 2241

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<212> DNA

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<223> 1 of 2 allelic variants (2242 is other entry)

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<222> (0)...(0)

<223> Accession number cg39462273

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51

<210> 2242

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<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2241 is other entry)

<221> misc\_feature  
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<223> Accession number cg39462273

<400> 2242  
gaacggacgc tgcctcctag tattaataaata cccaactctt tgatatctcc c 51

<210> 2243  
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<221> misc\_feature  
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<400> 2243  
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<210> 2244  
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<221> misc\_feature  
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<400> 2244  
atatacctta ttagcatttc ctttcaaaaa aaacagttgt ctttggattt t 51

<210> 2245  
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<221> misc\_feature

<222> (25)...(26)  
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<221> misc\_feature  
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<210> 2246  
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<223> 2 of 2 allelic variants (2245 is other entry)

<221> misc\_feature  
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<400> 2246  
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<210> 2247  
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<220>  
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<221> misc\_feature  
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<210> 2248  
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<221> misc\_feature  
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<400> 2248  
gtaagaactt ggtaggcagg ttgcgttgcc acacattcgc gatgaacgcg t 51

<210> 2249  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg39507328

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cgaggagaga ctaacttttc actttgtttc acctgtgatc tgggtctggc g 51

<210> 2250  
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<221> misc\_feature  
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<210> 2251  
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<221> misc\_feature  
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<223> Accession number cg39507822

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<210> 2252  
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<212> DNA  
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<223> Accession number cg39507822

<400> 2252  
tcagctttcc ttaagccctc ttccataaca aatgagacac ttacatgttt c 51

<210> 2253  
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<221> misc\_feature  
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<223> Accession number cg39507822

<400> 2253  
tcaaaattcc tagagtcaag atctgtttct tgactctggt gcaccgggag a 51

<210> 2254  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2253 is other entry)

<221> misc\_feature  
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<223> Accession number cg39507822

<400> 2254  
tcaaaattcc tagagtcaag atctgtttct tgactctggt gcaccgggag a 51

<210> 2255  
<211> 51  
<212> DNA  
<213> Homo sapiens

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<223> 1 of 2 allelic variants (2256 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39512670

<400> 2255

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<210> 2256

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2255 is other entry)

<221> misc\_feature

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<223> Accession number cg39512670

<400> 2256

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51

<210> 2257

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2258 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39515262

<400> 2257

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51

<210> 2258

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2257 is other entry)

<221> misc\_feature

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<223> Accession number cg39515262

<400> 2258  
cacttccac tgtgctctgc caagcgtctg tggagaggag ccctccacct g 51

<210> 2259  
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<223> 1 of 2 allelic variants (2260 is other entry)

<221> misc\_feature  
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<223> Accession number cg39515274

<400> 2259  
gagccatggc cgagccctgc tggggccggc gcgggcgga gcgggacgcg g 51

<210> 2260  
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<221> misc\_feature  
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<210> 2261  
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<220>  
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<223> 1 of 2 allelic variants (2262 is other entry)

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<400> 2261  
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<210> 2262  
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<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2261 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39515274

<400> 2262

gctttccagc ggccgggagg agcggatcct cggggccagg aaggtagcg c

51

<210> 2263

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2264 is other entry)

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<223> Accession number cg39515274

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51

<210> 2264

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2263 is other entry)

<221> misc\_feature

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<223> Accession number cg39515274

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<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (2266 is other entry)

<221> misc\_feature  
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<400> 2265  
ttcctctctt cgccctgccca accacttttt tagtttcttc tcctctctcg g 51

<210> 2266  
<211> 50  
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<221> misc\_feature  
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<221> misc\_feature  
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<210> 2267  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2268 is other entry)

<221> misc\_feature  
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<210> 2268  
<211> 51  
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<223> 2 of 2 allelic variants (2267 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg39516519

<400> 2268  
tagagcaggt acgcactgat ttgaaaagta gttggtgtgt ctcccatact g 51

<210> 2269  
<211> 51  
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<221> misc\_feature  
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<223> Accession number cg39517070

<400> 2269  
cagaaccagg acgattgctc cgaaggcccc accacgagga aggcagccag g 51

<210> 2270  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg39517070

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<210> 2271  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg39517771

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<210> 2272  
<211> 51  
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (2271 is other entry)

<221> misc\_feature  
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<223> Accession number cg39517771

<400> 2272  
acggctctct cgacggacag gtcggagttt tcttcgtgat gatcgtggca g 51

<210> 2273  
<211> 51  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg39517771

<400> 2273  
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<210> 2274  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2273 is other entry)

<221> misc\_feature  
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<223> Accession number cg39517771

<400> 2274  
ttgtcggttt ggcgatcatc gtcaccattt tccgttcccg tcgcaccact t 51

<210> 2275  
<211> 51

<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (2276 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39517771

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<210> 2276  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2275 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39517771

<400> 2276  
aaccggcttg ttcaacgtgg cctgggtcat gattgcggtg ccactggtgg t 51

<210> 2277  
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<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2278 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39521356

<400> 2277  
cccagagcaa gctgcggctc attcacggac ccctcagaac aggctggatg a 51

<210> 2278  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2277 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39521356

<400> 2278

cccagagcaa gctgcggctc attcatggac ccctcagaac aggctggatg a

51

<210> 2279

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2280 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39522018

<400> 2279

atactctgtg tgtctatgtg cttagcgggg aacctccaga ggaggtggtg a

51

<210> 2280

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2279 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39522018

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51

<210> 2281

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2282 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39523840

<400> 2281  
tggcattttt aagtcgtgta gaactcacia ctttttaaac accttcccat a 51

<210> 2282  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2281 is other entry)

<221> misc\_feature  
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<223> Accession number cg39523840

<400> 2282  
tggcattttt aagtcgtgta gaacttacia ctttttaaac accttcccat a 51

<210> 2283  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2284 is other entry)

<221> misc\_feature  
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<223> Accession number cg39524105

<400> 2283  
tcttgagacc aggcatagtg ctgggcactg gtgcaagcga agtggaagtc g 51

<210> 2284  
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<220>  
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<223> 2 of 2 allelic variants (2283 is other entry)

<221> misc\_feature  
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<223> Accession number cg39524105

<400> 2284  
tcttgagacc aggcatagtg ctgggtactg gtgcaagcga agtggaagtc g 51

<210> 2285  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2286 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39524138

<400> 2285

gctgacgaga tgatcgcccg cgacgggttc atctggcgca ggccttgagg a

51

<210> 2286

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2285 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39524138

<400> 2286

gctgacgaga tgatcgcccg cgacgagttc atctggcgca ggccttgagg a

51

<210> 2287

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2288 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39524138

<400> 2287

cgagatgatc gcccgcgacg gggtcatctg gcgcaggcct tgaggaggag a

51

<210> 2288

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2287 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39524138

<400> 2288  
cgagatgatc gccgcgcacg gggtcgtctg ggcaggcct tgaggaggag a 51

<210> 2289  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2290 is other entry)

<221> misc\_feature  
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<223> Accession number cg39524138

<400> 2289  
gatcgtcacg ctcaacgaca ccaccgcctc gaagattggt ggggccatcg t 51

<210> 2290  
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<212> DNA  
<213> Homo sapiens

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<221> misc\_feature  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39524138

<400> 2290  
gatcgtcacg ctcaacgaca ccaccctcg aagattggtg gggccatcgt 50

<210> 2291  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2292 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg39524138

<400> 2291  
aggcccgctcg taccgttggg tctggatctg ggttggttca caccctcatt t 51

<210> 2292  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2291 is other entry)

<221> misc\_feature  
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<223> Accession number cg39524138

<400> 2292  
aggcccgctcg taccgttggg tctgggtctg ggttggttca caccctcatt t 51

<210> 2293  
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<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2294 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39524728

<400> 2293  
agcccaccac cgccgggtac ctgcacagcc acatatatgc aagtacacac a 51

<210> 2294  
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<220>  
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<223> Accession number cg39524728

<400> 2294  
agcccaccac cgccgggtac ctgcaaagcc acatatatgc aagtacacac a 51

<210> 2295  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2296 is other entry)

<221> misc\_feature  
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<223> Accession number cg39524728

<400> 2295  
cacaggcact cgcacgcatg catgctcatg caacacacat gtacactcta c 51

<210> 2296  
<211> 51  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2295 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39524728

<400> 2296  
cacaggcact cgcacgcatg catgcccacat gtacactcta c 51

<210> 2297  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2298 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39524728

<400> 2297  
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<210> 2298  
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<210> 2299  
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<400> 2299  
cccacacaca aagtacacac acgtacacca tatgcatatg tatgcactca t 51

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<210> 2301  
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<221> misc\_feature  
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catatgtatg cactcataca ctcatacata tgtgccccct cagagaagta c

51

<210> 2302

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2301 is other entry)

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catatgtatg cactcataca ctcatgcata tgtgccccct cagagaagta c

51

<210> 2303

<211> 51

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<213> Homo sapiens

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<223> 1 of 2 allelic variants (2304 is other entry)

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caagacacaa acacatgtac acgcacacat gcgcacacac acgtacatct a

51

<210> 2304

<211> 51

<212> DNA

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caagacacaa acacatgtac acgcatacat gcgcacacac acgtacatct a

51

<210> 2305



<211> 51  
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<400> 2305  
gcgcgcctac cttgccagac cctgggcacg cctgccttca ggtgccagg c 51

<210> 2306  
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<210> 2307  
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gctacagcct gcagtcctga gcgtgaggtg ctatacttcc caggagacat c 51

<210> 2308  
<211> 51  
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<223> 2 of 2 allelic variants (2307 is other entry)

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<223> Accession number cg39530012

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51

<210> 2309

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2310 is other entry)

<221> misc\_feature

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<223> Accession number cg39530051

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51

<210> 2310

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2309 is other entry)

<221> misc\_feature

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<223> Accession number cg39530051

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<210> 2311

<211> 50

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2312 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39535156

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50

<210> 2312  
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<212> DNA  
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<223> 2 of 2 allelic variants (2311 is other entry)

<221> misc\_feature  
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<223> Accession number cg39535156

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51

<210> 2313  
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<223> 1 of 2 allelic variants (2314 is other entry)

<221> misc\_feature  
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<223> Accession number cg39535310

<400> 2313  
ttgaagcagg gcagtaaatt taccagcttc ttgatgaaac ataactccag t

51

<210> 2314  
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<221> misc\_feature

<222> (0)...(0)  
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<400> 2314  
ttgaagcagg gcagtaaatt taccaacttc ttgatgaaac ataactccag t 51

<210> 2315  
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<223> 1 of 2 allelic variants (2316 is other entry)

<221> misc\_feature  
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<400> 2315  
atactgctaa taaatgacag tggctgctaa catctcttga gcactgcct t 51

<210> 2316  
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<220>  
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<223> 2 of 2 allelic variants (2315 is other entry)

<221> misc\_feature  
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<400> 2316  
atactgctaa taaatgacag tggctactaa catctcttga gcactgcct t 51

<210> 2317  
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<220>  
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<400> 2317  
gaaggacag gacttggctg ctgattccat gtggaggagc tgctcacggt g 51

<210> 2318  
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<223> Accession number cg39535310  
  
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<210> 2319  
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<222> (0)...(0)  
<223> Accession number cg39536028  
  
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atcagtcaag ccgtcatgat catcgtggga aaagaagtaa ccaggcagaa t 51  
  
<210> 2320  
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<223> 2 of 2 allelic variants (2319 is other entry)  
  
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<222> (0)...(0)  
<223> Accession number cg39536028  
  
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<210> 2321  
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<221> misc\_feature  
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<221> misc\_feature  
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<400> 2321  
agcagggtgag ggtcactacc tctccttttc ctgcctgccc cggcctctcc c 51

<210> 2322  
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<221> misc\_feature  
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<400> 2322  
agcagggtgag ggtcactacc tctcattttc ctgcctgccc cggcctctcc c 51

<210> 2323  
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<221> misc\_feature  
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<400> 2323  
aaccatgggt ttagtgtcca ccagacttaa aggaccagg accttctcac c 51

<210> 2324  
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<221> misc\_feature  
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<223> Accession number cg39536028

<400> 2324

aaccatgggt ttagtgcca ccagatttaa aggaccagg accttctcac c

51

<210> 2325

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2326 is other entry)

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<222> (0)...(0)

<223> Accession number cg39537504

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caggtctgtg aagcttctgg gctcaggaga gtcttgccg acgcttgctc g

51

<210> 2326

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 2 of 2 allelic variants (2325 is other entry)

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<222> (0)...(0)

<223> Accession number cg39537504

<400> 2326

caggtctgtg aagcttctgg gctcaagaga gtcttgccg acgcttgctc g

51

<210> 2327

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39537504

<400> 2327  
tcgggaacct cgccatgccg cgcgcacctc cctaccccac cgcgcagtc 50

<210> 2328  
<211> 51  
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<221> misc\_feature  
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<400> 2328  
tcgggaacct cgccatgccg cgcgcgacct ccctacccca cgcgcagtc c 51

<210> 2329  
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<400> 2329  
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<210> 2330  
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<210> 2331  
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<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (2332 is other entry)

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51

<210> 2332

<211> 51

<212> DNA

<213> Homo sapiens

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acccacccg ccagtccttc gccggcgctc gggggctccc gatgcaatag g

51

<210> 2333

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2334 is other entry)

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<223> Accession number cg39540190

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51

<210> 2334

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2333 is other entry)

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tcagatccat gagagctgca aagttgcgga agcgtgagcg ccgctggagg a 51

<210> 2335  
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<221> misc\_feature  
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<400> 2335  
gaaagtcaag cagtgggaag tacatggagc tctcagccct gctcccatct g 51

<210> 2336  
<211> 51  
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<220>  
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<400> 2336  
gaaagtcaag cagtgggaag tacatagagc tctcagccct gctcccatct g 51

<210> 2337  
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<221> misc\_feature  
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<223> Accession number cg39540317

<400> 2337

tcagcagatg ggccactgac tgagcgctgc cccgtccctg gtgctactgg t

51

<210> 2338

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2337 is other entry)

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<223> Accession number cg39540317

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tcagcagatg ggccactgac tgagcactgc cccgtccctg gtgctactgg t

51

<210> 2339

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2340 is other entry)

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tgggccactg actgagcgct gcccgcctcc tgggtgctact ggtctttcta a

51

<210> 2340

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2339 is other entry)

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51

<210> 2341

<211> 51

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<400> 2341  
cccgtccctg gtgctactgg tcttttctaaa cttagcacc tggagagtcc a 51

<210> 2342  
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<220>  
<221> misc\_feature  
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<223> Accession number cg39540317

<400> 2342  
cccgtccctg gtgctactgg tctttttctaaa cttagcacc tggagagtcc a 51

<210> 2343  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2344 is other entry)

<221> misc\_feature  
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<400> 2343  
ggtgctactg gtcttttctaa acttagcacc ctggagagtc caaggaggca g 51

<210> 2344  
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<220>  
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<223> 2 of 2 allelic variants (2343 is other entry)

<221> misc\_feature  
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<223> Accession number cg39540317

<400> 2344  
ggtgctactg gtcttttctaa acttaacacc ctggagagtc caaggaggca g 51

<210> 2345  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2346 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39540409

<400> 2345  
catgttttct tcttgagaa agtgtcagaa aagtgtacag cctggggcca a 51

<210> 2346  
<211> 51  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg39540409

<400> 2346  
catgttttct tcttgagaa agtgtagaa aagtgtacag cctggggcca a 51

<210> 2347  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> Accession number cg39540537

<400> 2347  
actggcggca ggaatgaatc agcagatagt cattttcccg cagcccttct a 51

<210> 2348  
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<221> misc\_feature  
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<223> Accession number cg39540537

<400> 2348  
actggcggca ggaatgaatc agcaggtagt cattttcccg cagcccttct a

51

<210> 2349  
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<220>  
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<221> misc\_feature  
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<400> 2349  
ctttcccat tagattttgt gtgtgctgt gtttattatt ttggtaggcg g

51

<210> 2350  
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<220>  
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<221> misc\_feature  
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<400> 2350  
ctttcccat tagattttgt gtgtgtgtgt gtttattatt ttggtaggcg g

51

<210> 2351  
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<220>  
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<223> 1 of 2 allelic variants (2352 is other entry)

<221> misc\_feature  
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<223> Accession number cg39543172

<400> 2351  
cagcagccgg gagtagtgcc cgcttcccc acaggaagtt cctgtctgcg c 51

<210> 2352  
<211> 51  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg39543172

<400> 2352  
cagcagccgg gagtagtgcc cgcttgcccc acaggaagtt cctgtctgcg c 51

<210> 2353  
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<212> DNA  
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<221> misc\_feature  
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<223> Accession number cg39543172

<400> 2353  
agcagccggg agtagtgccc gcttccccca caggaagttc ctgtctgcgc c 51

<210> 2354  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2353 is other entry)

<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg39543172

<400> 2354  
agcagccggg agtagtgccc gcttcgccc caggaagttc ctgtctgcgc c 51

<210> 2355  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2356 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39543172

<400> 2355  
ggaagttcct gtctgcgccc acccaggggt tgggtgtgag cagcttctca g 51

<210> 2356  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2355 is other entry)

<221> misc\_feature  
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<223> Accession number cg39543172

<400> 2356  
ggaagttcct gtctgcgccc acccaggggt tgggtgtgag cagcttctca g 51

<210> 2357  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2358 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39543172

<400> 2357  
agcaagcccc acagctgtcc tgcacgagtg gaggtgtctc acacagccct t 51



<210> 2358  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2357 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39543172

<400> 2358  
agcaagcccc acagctgtcc tgcacaagtg gaggctgctc acacagccct t 51

<210> 2359  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2360 is other entry)

<221> misc\_feature  
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<223> Accession number cg39545387

<400> 2359  
gtagagaggg ccagtgtggt gcgattttgt gggaggagtt gagattggat g 51

<210> 2360  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2359 is other entry)

<221> misc\_feature  
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<223> Accession number cg39545387

<400> 2360  
gtagagaggg ccagtgtggt gcgatcttgt gggaggagtt gagattggat g 51

<210> 2361  
<211> 51  
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<220>

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<221> misc\_feature  
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<223> Accession number cg39545387

<400> 2361  
gtagaggagg aagtgactgt cggcaagtgt ggagagagga gccccagctt c 51

<210> 2362  
<211> 51  
<212> DNA  
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<221> misc\_feature  
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<223> Accession number cg39545387

<400> 2362  
gtagaggagg aagtgactgt cggcatgtgt ggagagagga gccccagctt c 51

<210> 2363  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2364 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39545387

<400> 2363  
cttcacctta atgtgaggct gattcgtgaa cccatttatt cttgtggcag a 51

<210> 2364  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2363 is other entry)

<221> misc\_feature  
<222> (0)...(0)

<223> Accession number cg39545387

<400> 2364

cttcacctta atgtgaggct gattcatgaa cccatttatt cttgtggcag a

51

<210> 2365

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (2366 is other entry)

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<223> Accession number cg39545619

<400> 2365

gaggggccga cgagctgggt ctgcgcaaag cagtgaaggc cgagtttggc g

51

<210> 2366

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2365 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39545619

<400> 2366

gaggggccga cgagctgggt ctgcgtaaag cagtgaaggc cgagtttggc g

51

<210> 2367

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2368 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39545619

<400> 2367

gccgacgagc tgggtctgcg caaagcagtg aaggccgagt ttggcggggg c

51

<210> 2368

<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2367 is other entry)

<221> misc\_feature  
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<400> 2368  
gccgacgagc tgggtctgcg caaagtagtg aaggccgagt ttggcggggg c

51

<210> 2369  
<211> 51  
<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2370 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39545619

<400> 2369  
agtgaaggcc gagtttggcg ggggcacccg cggcttctcc tgcgaggagg a

51

<210> 2370  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2369 is other entry)

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<223> Accession number cg39545619

<400> 2370  
agtgaaggcc gagtttggcg ggggcgcccg cggcttctcc tgcgaggagg a

51

<210> 2371  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (26)...(0)  
<223> 1 of 2 allelic variants (2372 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39545619

<400> 2371  
gctgcagaat ttgcgtgccca agcagggaga agcactccac aacgtgcgct t 51

<210> 2372  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (2371 is other entry)

<221> misc\_feature  
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<223> Accession number cg39545619

<400> 2372  
gctgcagaat ttgcgtgccca agcagagaga agcactccac aacgtgcgct t 51

<210> 2373  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2374 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39545648

<400> 2373  
ctagagtata attaaggaga ctgcctgtgc ttgctgctgg aggggtgatg t 51

<210> 2374  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2373 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39545648

<400> 2374  
ctagagtata attaaggaga ctgcccgtgc ttgctgctgg aggggtgatg t 51

<210> 2375  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2376 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26.

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39559225

<400> 2375  
tccagcttta aaaaaaacac acacaaaact ttgccacagt gttgcatgag 50

<210> 2376  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2375 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39559225

<400> 2376  
tccagcttta aaaaaaacac acacacaaac ttgccacag tgttgcatga g 51

<210> 2377  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2378 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39559225

<400> 2377

aaaactttgc cacagtgttg catgagaata tgcttgcttt catgtgctgg c

51

<210> 2378

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2377 is other entry)

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<223> Accession number cg39559225

<400> 2378

aaaactttgc cacagtgttg catgaaaata tgcttgcttt catgtgctgg c

51

<210> 2379

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2380 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39559767

<400> 2379

gcaaaccggg catggagacc ccatctcagg tctgtgcttc tctgggggcc a

51

<210> 2380

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2379 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39559767

<400> 2380

gcaaaccggg catggagacc ccatcccagg tctgtgcttc tctgggggcc a

51

<210> 2381

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2382 is other entry)

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<222> (0)...(0)  
<223> Accession number cg39560753

<400> 2381  
tcggctgtct tctgctgccg gcaggaacgg ggctcaacc ttctctgggc a 51

<210> 2382  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2381 is other entry)

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<222> (0)...(0)  
<223> Accession number cg39560753

<400> 2382  
tcggctgtct tctgctgccg gcaggtacgg ggctcaacc ttctctgggc a 51

<210> 2383  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2384 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39564627

<400> 2383  
gaggagccca gaacactggg ggctgtgcta ctagcaccat agaattcagg t 51

<210> 2384  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
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<400> 2384  
gaggagccca gaacactggg ggctggctac tagcaccata gaattcaggt

50

<210> 2385  
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<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (2386 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 2385  
cataacaagg cgtaggggtat ggggtgacat ttctacattg cagcagcaca t

51

<210> 2386  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2385 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 2386  
cataacaagg cgtaggggtat ggggtaacat ttctacattg cagcagcaca t

51

<210> 2387  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2388 is other entry)

<221> misc\_feature  
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<223> Accession number cg39564709

<400> 2387

gttggtcagt gggggtgggc ctgggcctaa cttttcaagc tgaagatgct c

51

<210> 2388

<211> 50

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2387 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39564709

<400> 2388

gttggtcagt gggggtgggc ctgggcctaac ttttcaagct gaagatgctc

50

<210> 2389

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2390 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39565239

<400> 2389

tcaagggacc cgaagactag gggagaagca gcgagcgggt cgcggccgcc t

51

<210> 2390

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2389 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39565239

<400> 2390  
tcaagggacc cgaagactag gggaggagca gcgagcgggt cgcggccgcc t 51

<210> 2391  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2392 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39571018

<400> 2391  
cctctggtcc cggtgctaag agcagggttg gtctgcagc ttcttggtg c 51

<210> 2392  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2391 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39571018

<400> 2392  
cctctggtcc cggtgctaag agcagagttg gtctgcagc ttcttggtg c 51

<210> 2393  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2394 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39571022

<400> 2393  
ctgcatccgc tgggtggcaga gacacagttg ggggaggcag aggtggcact g 51

<210> 2394  
<211> 51  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2393 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39571022

<400> 2394

ctgcatccgc tgggtggcaga gacacggttg ggggaggcag aggtggcact g

51

<210> 2395

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2396 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39574041

<400> 2395

tttgggaggc cgaggcgggc ggatgacaag atcaggagtt tgagaccagc c

51

<210> 2396

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2395 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39574041

<400> 2396

tttgggaggc cgaggcgggc ggatggcaag atcaggagtt tgagaccagc c

51

<210> 2397

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2398 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39574041

<400> 2397  
tgggaggccg aggcgggcgg atgacaagat caggagttag agaccagcct g 51

<210> 2398  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2397 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39574041

<400> 2398  
tgggaggccg aggcgggcgg atgacgagat caggagttag agaccagcct g 51

<210> 2399  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2400 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39575681

<400> 2399  
gcattgggtc tgccccgata gtcggggcgt aggggtgcca gacatgacgt c 51

<210> 2400  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2399 is other entry)

<221> misc\_feature  
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<223> Accession number cg39575681

<400> 2400

gcattggggtc tgccccgatc gtcggtgctg aggggtgccca gacatgacgt c

51

<210> 2401

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2402 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39575791

<400> 2401

agcacacaaa tgcccacgta tgtgcatgca tgaaaacaca tgaaacacac a

51

<210> 2402

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2401 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39575791

<400> 2402

agcacacaaa tgcccacgta tgtgcgtgca tgaaaacaca tgaaacacac a

51

<210> 2403

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2404 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39575791

<400> 2403

gcacacgtgc acacacacag ccacatgcac acatccacac gcacgcacac a

51

<210> 2404

<211> 51

<212> DNA

<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2403 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39575791

<400> 2404  
gcacacgtgc acacacacag ccacacgcac acatccacac gcacgcacac a 51

<210> 2405  
<211> 45  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2406 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39575852

<400> 2405  
gatgcggacc tcagtggcct gcaggcgag cggaagcca gcggt 45

<210> 2406  
<211> 44  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2405 is other entry)

<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 2406  
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<210> 2407  
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<221> misc\_feature  
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<223> Accession number cg39575854

<400> 2407  
gacgccgcga cttccggaag attctcgggg ttcgtgtagc taccagggc g . 51

<210> 2408  
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<221> misc\_feature  
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<223> Accession number cg39575854

<400> 2408  
gacgccgcga cttccggaag attcttgggg ttcgtgtagc taccagggc g 51

<210> 2409  
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<220>  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39575897

<400> 2409  
ctctgttaag ctctcacca gccatcttcc cagcgctct ctccctggg c 51

<210> 2410  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2409 is other entry)

<221> misc\_feature  
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<223> Accession number cg39575897

<400> 2410

ctctgttaag ctctcacca gccattttcc cagcgctct ctccctggg c

51

<210> 2411

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2412 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39581994

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gagatcaaga ccattcctggc taacacaggg aaaaccccgct ctctattaaa a

51

<210> 2412

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2411 is other entry)

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<223> Accession number cg39581994

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gagatcaaga ccattcctggc taacataggg aaaaccccgct ctctattaaa a

51

<210> 2413

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2414 is other entry)

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<223> Accession number cg39581994

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ctagcctgac ctgactgtta gaggccaat cactgtaagc caccaagctg c

51

<210> 2414

<211> 51  
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<221> misc\_feature  
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<210> 2415  
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<221> misc\_feature  
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<210> 2416  
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<220>  
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<223> 2 of 2 allelic variants (2415 is other entry)

<221> misc\_feature  
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<210> 2417  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2418 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39582195

<400> 2417  
gttcactgtg aaagcattct gcacccccac aactccgcct ctggcctggc c 51

<210> 2418  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2417 is other entry)

<221> misc\_feature  
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<223> Accession number cg39582195

<400> 2418  
gttcactgtg aaagcattct gcacctccac aactccgcct ctggcctggc c 51

<210> 2419  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2420 is other entry)

<221> misc\_feature  
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<223> Accession number cg39584802

<400> 2419  
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<210> 2420  
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<221> misc\_feature  
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<221> misc\_feature  
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<223> Accession number cg39584802

<400> 2420  
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<210> 2421  
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<223> 1 of 2 allelic variants (2422 is other entry)

<221> misc\_feature  
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<223> Accession number cg39584802

<400> 2421  
gaaaccaata cgaagataaa atgggaaaaa aaaaatccca ttcacggcac a 51

<210> 2422  
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<212> DNA  
<213> Homo sapiens

<220>  
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<221> misc\_feature  
<222> (25)...(26)  
<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 2422  
gaaaccaata cgaagataaa atgggaaaaa aaaatcccat tcacggcaca 50

<210> 2423  
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<220>  
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<221> misc\_feature

<222> (0)...(0)  
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<400> 2423  
acgaagataa aatgggaaaa aaaaaatccc attcacggca cagcctgccg a 51

<210> 2424  
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<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (2423 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39584802

<400> 2424  
acgaagataa aatgggaaaa aaaaaatccca ttcacggcac agcctgccga 50

<210> 2425  
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<220>  
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<223> 1 of 2 allelic variants (2426 is other entry)

<221> misc\_feature  
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<223> Accession number cg39585484

<400> 2425  
agacatggac ccacacacaa acatatgtgg acacacatgt acaaacatgc a 51

<210> 2426  
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<213> Homo sapiens

<220>  
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<223> 2 of 2 allelic variants (2425 is other entry)

<221> misc\_feature  
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<223> Accession number cg39585484

<400> 2426  
agacatggac ccacacacaa acatacgtgg acacacatgt acaaacatgc a 51

<210> 2427  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2428 is other entry)

<221> misc\_feature  
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<223> Accession number cg39587361

<400> 2427  
cacatgcata catgcccaca cacacactca tacaggtata cacacccata t 51

<210> 2428  
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<220>  
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<223> 2 of 2 allelic variants (2427 is other entry)

<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<223> Accession number cg39587361

<400> 2428  
cacatgcata catgcccaca cacacctcat acaggtatac acacccata 50

<210> 2429  
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<212> DNA  
<213> Homo sapiens

<220>  
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<223> 1 of 2 allelic variants (2430 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39587933

<400> 2429

acacagccag aatacagcaa atacagaggc gaatgccagc agcaaaccac t

51

<210> 2430

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 2 of 2 allelic variants (2429 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39587933

<400> 2430

acacagccag aatacagcaa atacataggc gaatgccagc agcaaaccac t

51

<210> 2431

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

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<223> 1 of 2 allelic variants (2432 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39587933

<400> 2431

agccagaata cagcaaatac agaggcgaat gccagcagca aaccactgaa c

51

<210> 2432

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2431 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39587933

<400> 2432

agccagaata cagcaaatac agagggtgaat gccagcagca aaccactgaa c

51

<210> 2433

<211> 51

<212> DNA

<213> Homo sapiens

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<210> 2434  
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<220>  
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<223> 2 of 2 allelic variants (2433 is other entry)

<221> misc\_feature  
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cagcagcaaa ccactgaact gagaacaggt cccctattga aggaatcaga g 51

<210> 2435  
<211> 51  
<212> DNA  
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<220>  
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<223> 1 of 2 allelic variants (2436 is other entry)

<221> misc\_feature  
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<223> Accession number cg39587933

<400> 2435  
agcaaaccac tgaactgaga ataggtcccc tattgaagga atcagagaaa g 51

<210> 2436  
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<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (2435 is other entry)



<221> misc\_feature  
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<400> 2436  
agcaaaccac tgaactgaga ataggacccc tattgaagga atcagagaaa g 51

<210> 2437  
<211> 51  
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<213> Homo sapiens

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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2438 is other entry)

<221> misc\_feature  
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<223> Accession number cg39587933

<400> 2437  
accactgaac tgagaatagg tcccctattg aaggaatcag agaaagaact g 51

<210> 2438  
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<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (2437 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
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<400> 2438  
accactgaac tgagaatagg tccccattg aaggaatcag agaaagaact g 51

<210> 2439  
<211> 51  
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<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2440 is other entry)

<221> misc\_feature  
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<223> Accession number cg39587933

<400> 2439  
cccctattga aggaatcaga gaaagaactg gaagagcttg aaggggctcg a 51

<210> 2440  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2439 is other entry)

<221> misc\_feature  
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<223> Accession number cg39587933

<400> 2440  
cccctattga aggaatcaga gaaaggactg gaagagcttg aaggggctcg a 51

<210> 2441  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2442 is other entry)

<221> misc\_feature  
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<223> Accession number cg39587933

<400> 2441  
tcgagacccc aaaagtacaa caatgccaaag caaccagagc ttccagggac t 51

<210> 2442  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2441 is other entry)

<221> misc\_feature  
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<223> Accession number cg39587933

<400> 2442  
tcgagacccc aaaagtacaa caatgtcaag caaccagagc ttccagggac t 51

<210> 2443  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2444 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39587933

<400> 2443  
ccaaaagtac aacaatgcca agcaaccaga gcttccaggg actaagccac t 51

<210> 2444  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2443 is other entry)

<221> misc\_feature  
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<223> Accession number cg39587933

<400> 2444  
ccaaaagtac aacaatgcca agcaatcaga gcttccaggg actaagccac t 51

<210> 2445  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2446 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39592883

<400> 2445  
ttgtcacttt tgctttcaga gtcactgctg ctgtaataat ccttgatcat g 51

<210> 2446  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2445 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39592883

<400> 2446

ttgtcacttt tgctttcaga gtcaccgctg ctgtaataat ccttgtagat g

51

<210> 2447

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2448 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

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<222> (0)...(0)

<223> Accession number cg39597328

<400> 2447

ttcttcctat actacaattt tttttcattt ttttcctaat gtagcgaagc

50

<210> 2448

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2447 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39597328

<400> 2448

ttcttcctat actacaattt ttttttcatt ttttcctaa ttagcgaag c

51

<210> 2449

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2450 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39597389

<400> 2449  
ttgggggact agaggagga tagcattagg agaaatacct aaaaaaagaa a 51

<210> 2450  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2449 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39597389

<400> 2450  
ttgggggact agaggagga tagcactagg agaaatacct aaaaaaagaa a 51

<210> 2451  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2452 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39597389

<400> 2451  
ttcccttttg agtcctgaac cccgacgtgc aaaaccatcc cttatcgatg a 51

<210> 2452  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 2 of 2 allelic variants (2451 is other entry)

<221> misc\_feature  
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<223> Accession number cg39597389

<400> 2452  
ttcccttttg agtcctgaac cccgatgtgc aaaaccatcc cttatcgatg a 51

<210> 2453  
<211> 44

<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2454 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39602141

<400> 2453  
gagggctagt ccagccttgt acaggctccg cccttgacac cggt

44

<210> 2454  
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<212> DNA  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2453 is other entry)

<221> misc\_feature  
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<223> Accession number cg39602141

<400> 2454  
gagggctagt ccagccttgt acagggtccg cccttgacac cggt

44

<210> 2455  
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<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2456 is other entry)

<221> misc\_feature  
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<223> Accession number cg39602254

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51

<210> 2456  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2455 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39602254

<400> 2456

gagacagggt ttcacatgt tgaccagggt ggtctcgaac tcctgacctc a

51

<210> 2457

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2458 is other entry)

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<222> (0)...(0)

<223> Accession number cg39602496

<400> 2457

cctccgggtcc agacctcgcc ccagggttgc ccagagatgt aatccaggct a

51

<210> 2458

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2457 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39602496

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cctccgggtcc agacctcgcc ccagggttgc ccagagatgt aatccaggct a

51

<210> 2459

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2460 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39607243

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atgctgtgtg tgtgtgtgtg tgtgtttttt gggggatgtg ggggcctgga 50

<210> 2460  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2459 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg39607243

<400> 2460  
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<210> 2461  
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<400> 2461  
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<210> 2462  
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<223> 2 of 2 allelic variants (2461 is other entry)

<221> misc\_feature  
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<223> Accession number cg39607243

<400> 2462

gtgtgtgtgt gtgtgtgtgt ttttttgggg gatgtggggg cctggagcct g

51

<210> 2463

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<212> DNA

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<223> 1 of 2 allelic variants (2464 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39607270

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51

<210> 2464

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2463 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39607270

<400> 2464

ccccagcggc ctggcgccca tggcaattcg gcagccgctc accgatactc g

51

<210> 2465

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2466 is other entry)

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<223> Accession number cg39612908

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51

<210> 2466

<211> 51  
<212> DNA  
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<223> Accession number cg39612908

<400> 2466  
tctatgcagg acgccggttc tgaagctgac agatacacca tcaatgagca a 51

<210> 2467  
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<212> DNA  
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<223> 1 of 2 allelic variants (2468 is other entry)

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<222> (0)...(0)  
<223> Accession number cg39612908

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<210> 2468  
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<223> Accession number cg39612908

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<210> 2469  
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<213> Homo sapiens

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<223> 1 of 2 allelic variants (2470 is other entry)

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<210> 2470

<211> 51

<212> DNA

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<223> Accession number cg39660253

<400> 2470

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<210> 2471

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2472 is other entry)

<221> misc\_feature

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<223> Accession number cg39660253

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<213> Homo sapiens

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<223> 2 of 2 allelic variants (2471 is other entry)

<221> misc\_feature  
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<210> 2473  
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<221> misc\_feature  
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<210> 2474  
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<221> misc\_feature  
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<400> 2474  
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<210> 2475  
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<221> misc\_feature  
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<223> Accession number cg39666355

<400> 2475

ccaccgtacc tggccctttt tttttatattt ttaagacaag gtattgctct g 51

<210> 2476

<211> 50

<212> DNA

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<223> Accession number cg39666355

<400> 2476

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<210> 2477

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2478 is other entry)

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<223> Accession number cg39667412

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<210> 2478

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2477 is other entry)

<221> misc\_feature

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<223> Accession number cg39667412

<400> 2478

tgtgtttcca caccgagga tgtgtaggcg ggtgcatgtg caccatggcg t 51

<210> 2479

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2480 is other entry)

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<222> (0)...(0)

<223> Accession number cg39667412

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cacgtgcacc atggcgtgca cacaaggggg actgtcaatc acaggctttc a

51

<210> 2480

<211> 50

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<223> Accession number cg39667412

<400> 2480

cacgtgcacc atggcgtgca cacaagggga ctgtcaatca caggctttca

50

<210> 2481

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2482 is other entry)

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<223> Accession number cg39667412

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51

<210> 2482

<211> 50

<212> DNA

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<223> Accession number cg39667412

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tgcaccatgg cgtgcacaca aggggactgt caatcacagg ctttcatatg

50

<210> 2483

<211> 51

<212> DNA

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<223> 1 of 2 allelic variants (2484 is other entry)

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<223> Accession number cg39704218

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51

<210> 2484

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<223> Accession number cg39704218

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<210> 2485

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<210> 2487  
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<210> 2488  
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<223> Accession number cg39706539

<400> 2488  
ttacaagcag ctgggcttgg tggctgatgc ctataatccc agcacttta a 51

<210> 2489  
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<220>  
<221> misc\_feature  
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<223> 1 of 2 allelic variants (2490 is other entry)

<221> misc\_feature  
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<223> Accession number cg39706617

<400> 2489  
catattcttc acctagcttc caaaacctat acttctctcg gcttttctct g 51

<210> 2490  
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<221> misc\_feature  
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<400> 2490  
catattcttc acctagcttc caaaatctat acttctctcg gcttttctct g 51

<210> 2491  
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<223> 1 of 2 allelic variants (2492 is other entry)

<221> misc\_feature  
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<223> Accession number cg39707457

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<223> Accession number cg39707457  
  
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<210> 2494  
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<223> Accession number cg39707457  
  
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<210> 2495  
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<223> 1 of 2 allelic variants (2496 is other entry)

<221> misc\_feature  
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<210> 2496  
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<221> misc\_feature  
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gctcgccgac gccgccgatg cccttcccg tgcaaaggtg cgcgcgaccg t 51

<210> 2497  
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<221> misc\_feature  
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aggctgtcgc cactcagtgc attgccggcc tggcatgtgg tcgcccgatt c 51

<210> 2498  
<211> 51  
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<221> misc\_feature

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<400> 2498

aggctgtcgc cactcagtgc attgctggcc tggcatgtgg tcgcccgatt c

51

<210> 2499

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<210> 2500

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51

<210> 2501

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2502 is other entry)

<221> misc\_feature

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<223> Accession number cg39708746

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51

<210> 2502  
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<221> misc\_feature  
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<210> 2504  
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<223> 2 of 2 allelic variants (2503 is other entry)

<221> misc\_feature  
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<223> Accession number cg39709129

<400> 2504  
gttggcagcc attcatggag ggtgcctacc tgaaattggt gctcttgcc t 51

<210> 2505  
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<212> DNA  
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<221> misc\_feature  
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<223> Accession number cg39711126

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<210> 2506  
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<221> misc\_feature  
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<223> Accession number cg39711126

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<221> misc\_feature  
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<223> Accession number cg39714236

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<210> 2508  
<211> 51  
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<223> 2 of 2 allelic variants (2507 is other entry)

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<400> 2508

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51

<210> 2509

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<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2510 is other entry)

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<223> Accession number cg39716704

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51

<210> 2510

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

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<223> 2 of 2 allelic variants (2509 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39716704

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<210> 2511

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<212> DNA

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<223> 1 of 2 allelic variants (2512 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg39721166

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<210> 2512  
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<210> 2513  
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<221> misc\_feature  
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<223> Accession number cg39726191

<400> 2513  
tactgaacag ccctttggaa ctctgaatga tttgggcctc acagaagctc c 51

<210> 2514  
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<210> 2515  
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<210> 2516

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<223> 2 of 2 allelic variants (2515 is other entry)

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51

<210> 2517

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<223> Accession number cg39731647

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51

<210> 2518

<211> 50

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<210> 2520  
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<210> 2524  
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50

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51

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<210> 2527  
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<210> 2533  
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51

<210> 2534

<211> 50

<212> DNA

<213> Homo sapiens

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50

<210> 2535

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<212> DNA

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51

<210> 2536

<211> 51

<212> DNA

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<223> 2 of 2 allelic variants (2535 is other entry)

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51

<210> 2538

<211> 51

<212> DNA

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<211> 51

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51

<210> 2540

<211> 51

<212> DNA

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acagtgagcc aagattgtgc cactgcactc cagcctgggc gacagagtga g 51

<210> 2542  
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51

<210> 2544

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51

<210> 2545

<211> 51

<212> DNA

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<210> 2546

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51

<210> 2547

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<221> misc\_feature  
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<210> 2548  
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ccttgattat gtgagtaatg cgagtacctg gttgtttcag ttgaaggtgc t 51

<210> 2552  
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ccttgattat gtgagtaatg cgagtgcctg gttgtttcag ttgaaggtgc t 51

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agttgaaggt gctgtattga cttgcccttt tcattcctct ccatgagagc c 51

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<210> 2555  
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<400> 2555  
gcaggagaag acctccttgt tcccatggct catggccacg ttgctcccat c 51

<210> 2556  
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<400> 2556

gcaggagaag acctccttgt tcccacggct catggccacg ttgctcccat c

51

<210> 2557

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2558 is other entry)

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<223> Accession number cg40307796

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51

<210> 2558

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<223> Accession number cg40307796

<400> 2558

cactggtctc aggtcgctgc cctccatttc ctcttctggg agtggaggct c

51

<210> 2559

<211> 51

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<223> 1 of 2 allelic variants (2560 is other entry)

<221> misc\_feature

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<223> Accession number cg40312834

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51

<210> 2560

<211> 50

<212> DNA

<213> Homo sapiens

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<221> misc\_feature  
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<210> 2561  
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<213> Homo sapiens

<220>  
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<221> misc\_feature  
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<223> Accession number cg40329454

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<210> 2562  
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<223> 2 of 2 allelic variants (2561 is other entry)

<221> misc\_feature  
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<210> 2563  
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<221> misc\_feature  
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<210> 2564  
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<400> 2564  
taacataagc agtgaaaatg agacagtgga gtatgggaag caaaaaataa g 51

<210> 2565  
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<223> Accession number cg40341796

<400> 2565  
tgaaaatgag acaatggagt atgggaagca aaaaataagt cattaggcag a 51

<210> 2566  
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<220>  
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<223> Accession number cg40341796

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51

<210> 2567

<211> 51

<212> DNA

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<223> Accession number cg40381397

<400> 2567

cttgtagttg ctggtacaa acctgggcct ccacaatggc aatgggggag t

51

<210> 2568

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2567 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg40381397

<400> 2568

cttgtagttg ctggtacaa acctgtgcct ccacaatggc aatgggggag t

51

<210> 2569

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2570 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg40385017

<400> 2569

aaaacttaaa gtataataaa aaaaaattta tattaaatta atctgtatgt g

51

<210> 2570

<211> 50  
<212> DNA  
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<220>  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg40385017

<400> 2570  
aaaacttaaa gtataataaa aaaaatttat attaaattaa tctgtatgtg

50

<210> 2571  
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<223> 1 of 2 allelic variants (2572 is other entry)

<221> misc\_feature  
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<223> Accession number cg40389166

<400> 2571  
tgctgggacc acaggcgtga gcccctgcac ccggcctgat ttacatcatt t

51

<210> 2572  
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<213> Homo sapiens

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<223> 2 of 2 allelic variants (2571 is other entry)

<221> misc\_feature  
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<223> Accession number cg40389166

<400> 2572  
tgctgggacc acaggcgtga gccccgcac ccggcctgat ttacatcatt t

51

<210> 2573  
<211> 51  
<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2574 is other entry)

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<223> Accession number cg40389419

<400> 2573

aaggttcaaa gtttcaataa atcccggaaa actacattcc taaaggctgt g

51

<210> 2574

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2573 is other entry)

<221> misc\_feature

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<223> Accession number cg40389419

<400> 2574

aaggttcaaa gtttcaataa atcccagaaa actacattcc taaaggctgt g

51

<210> 2575

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2576 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg40790872

<400> 2575

tctactaaaa atacaaaaat tagccaggca tgggtggcagg cacctgtagt c

51

<210> 2576

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

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<223> 2 of 2 allelic variants (2575 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg40790872

<400> 2576  
tctactaaaa atacaaaaat tagccgggca tgggtggcagg cacctgtagt c 51

<210> 2577  
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<223> 1 of 2 allelic variants (2578 is other entry)

<221> misc\_feature  
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<223> Accession number cg40790872

<400> 2577  
aaattagcca ggcattggtgg caggcacctg tagtcccagc tactcgggag g 51

<210> 2578  
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<221> misc\_feature  
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<223> Accession number cg40790872

<400> 2578  
aaattagcca ggcattggtgg caggcgctg tagtcccagc tactcgggag g 51

<210> 2579  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2580 is other entry)

<221> misc\_feature  
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<223> Accession number cg40797606

<400> 2579

tccggccgtg ggcgccagaa gcgggtgtgt aaatatgtgt gaacaagcgc t

51

<210> 2580

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 2 of 2 allelic variants (2579 is other entry)

<221> misc\_feature

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<223> Accession number cg40797606

<400> 2580

tccggccgtg ggcgccagaa gcgggcgtgt aaatatgtgt gaacaagcgc t

51

<210> 2581

<211> 51

<212> DNA

<213> Homo sapiens

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<223> 1 of 2 allelic variants (2582 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg40797606

<400> 2581

acatgcttta agacttgact tcggggaaaa aaaaaaaaaa aaattttttt t

51

<210> 2582

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2581 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg40797606

<400> 2582

acatgcttta agacttgact tcgggaaaaa aaaaaaaaaa aaattttttt t

51

<210> 2583

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2584 is other entry)

<221> misc\_feature  
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<223> Accession number cg40885230

<400> 2583  
cctgggcctc cagctgctgc agaaggatgc cgccgccgcc cctgccaccc c 51

<210> 2584  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg40885230

<400> 2584  
cctgggcctc cagctgctgc agaagaatgc cgccgccgcc cctgccaccc c 51

<210> 2585  
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<220>  
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<223> 1 of 2 allelic variants (2586 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg40927039

<400> 2585  
gcgttcttcg gcatcttctt tggggccctg ggcggcctct tgctgctggg g 51

<210> 2586  
<211> 51  
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<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2585 is other entry)

<221> misc\_feature  
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<223> Accession number cg40927039

<400> 2586  
gcgttcttcg gcattctctt tggggtcctg ggcggcctct tgctgctggg g 51

<210> 2587  
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<212> DNA  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2588 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg40932131

<400> 2587  
tgaaagaagc ttttaacacc tgaaagtcac ctcaaaatgg atatatgggt a 51

<210> 2588  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (2587 is other entry)

<221> misc\_feature  
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<223> Accession number cg40932131

<400> 2588  
tgaaagaagc ttttaacacc tgaaaatcat ctcaaaatgg atatatgggt a 51

<210> 2589  
<211> 51  
<212> DNA  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2590 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg40949022

<400> 2589  
tcagagacca gcccgcccaa catggcgaaa ccccgctctc actaaaaata c 51

<210> 2590

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2589 is other entry)

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<223> Accession number cg40949022

<400> 2590

tcagagacca gcccgccaa catggtgaaa cccgtctcc actaaaaata c

51

<210> 2591

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2592 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg40949022

<400> 2591

cagcccgcc aacatggcga aaccctgtct ccactaaaaa tacaaaaaat c

51

<210> 2592

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2591 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg40949022

<400> 2592

cagcccgcc aacatggcga aaccctgtct ccactaaaaa tacaaaaaat c

51

<210> 2593

<211> 51

<212> DNA

<213> Homo sapiens



<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2594 is other entry)

<221> misc\_feature  
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<223> Accession number cg40949022

<400> 2593  
ggccaacatg gcgaaacccc gtctccacta aaaatacaaaa aaatcagcca g 51

<210> 2594  
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<220>  
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<223> 2 of 2 allelic variants (2593 is other entry)

<221> misc\_feature  
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<223> Accession number cg40949022

<400> 2594  
ggccaacatg gcgaaacccc gtctctacta aaaatacaaaa aaatcagcca g 51

<210> 2595  
<211> 51  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2596 is other entry)

<221> misc\_feature  
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<223> Accession number cg40987225

<400> 2595  
caacatggca aaaccccatc tctacaaaaa atacaaaaag attagccagg c 51

<210> 2596  
<211> 51  
<212> DNA  
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<220>  
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<221> misc\_feature

<222> (0)...(0)  
<223> Accession number cg40987225

<400> 2596  
caacatggca aaaccccatc tctactaaaa atacaaaaag attagccagg c 51

<210> 2597  
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<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2598 is other entry)

<221> misc\_feature  
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<223> Accession number cg40999240

<400> 2597  
ttcgccatgt tggccaggct ggtcttgacc tctgagctc aagagatcca c 51

<210> 2598  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> 2 of 2 allelic variants (2597 is other entry)

<221> misc\_feature  
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<223> Accession number cg40999240

<400> 2598  
ttcgccatgt tggccaggct ggtctcgacc tctgagctc aagagatcca c 51

<210> 2599  
<211> 51  
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<220>  
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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2600 is other entry)

<221> misc\_feature  
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<223> Accession number cg41038983

<400> 2599  
cgcttccccg ctcagcgcac tcagtttgcg gctgggaatg accctcgccg c 51

<210> 2600

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2599 is other entry)

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<222> (0)...(0)

<223> Accession number cg41038983

<400> 2600

cgcttccccg ctcagcgcac tcagtctgcg gctgggaatg accctcgccg c

51

<210> 2601

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2602 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg41060726

<400> 2601

caatgggcaa atacacattt tcttggtatt ctccacaaga ataaactaat a

51

<210> 2602

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 2 of 2 allelic variants (2601 is other entry)

<221> misc\_feature

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<223> Accession number cg41060726

<400> 2602

caatgggcaa atacacattt tcttgatatt ctccacaaga ataaactaat a

51

<210> 2603

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2604 is other entry)

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg41060726

<400> 2603  
catctcttac cctctaaaaa aaaaaaggca attatttttaa ttccctgtaa t 51

<210> 2604  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg41060726

<400> 2604  
catctcttac cctctaaaaa aaaaaggcaa ttatttttaat tccttgtaat 50

<210> 2605  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2606 is other entry)

<221> misc\_feature  
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<223> Accession number cg41066315

<400> 2605  
aggccgcttt ccccttcttc tcgccctgcg gcagagagcg caacttctg c 51

<210> 2606  
<211> 50  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (2605 is other entry)

<221> misc\_feature

<222> (25)...(26)

<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg41066315

<400> 2606

aggccgcttt ccccttcctc tcgcctgcgg cagagagcgc aacttcctgc

50

<210> 2607

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2608 is other entry)

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<222> (0)...(0)

<223> Accession number cg41066315

<400> 2607

ctcctactgc ggcggtggcg aggcctggc cgtgcccttc gagccggcgc g

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<210> 2608

<211> 50

<212> DNA

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<221> misc\_feature

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50

<210> 2609

<211> 51

<212> DNA

<213> Homo sapiens

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<221> misc\_feature  
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<223> Accession number cg41066315

<400> 2609  
actgcggcgg tggcgaggcc ctggccgtgc ccttcgagcc ggcgcgcctg c 51

<210> 2610  
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<221> misc\_feature  
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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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<400> 2610  
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<210> 2611  
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<213> Homo sapiens

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<222> (26)...(0)  
<223> 1 of 2 allelic variants (2612 is other entry)

<221> misc\_feature  
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<223> Accession number cg41079413

<400> 2611  
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<210> 2612  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
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<223> 2 of 2 allelic variants (2611 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg41079413

<400> 2612

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51

<210> 2613

<211> 51

<212> DNA

<213> Homo sapiens

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2614 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg41079413

<400> 2613

cttagacctc atgatgtctg gaatgtgacc tgggagatgc tgcagcctcc a

51

<210> 2614

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2613 is other entry)

<221> misc\_feature

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<223> Accession number cg41079413

<400> 2614

cttagacctc atgatgtctg gaatgggacc tgggagatgc tgcagcctcc a

51

<210> 2615

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 1 of 2 allelic variants (2616 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg41084544

<400> 2615  
acaggcatgc accaccatgc ccggctaatt ttgtattttt agtggagacg g 51

<210> 2616  
<211> 51  
<212> DNA  
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<220>  
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<223> 2 of 2 allelic variants (2615 is other entry)

<221> misc\_feature  
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<223> Accession number cg41084544

<400> 2616  
acaggcatgc accaccatgc ccggccaatt ttgtattttt agtggagacg g 51

<210> 2617  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (26)...(0)  
<223> 1 of 2 allelic variants (2618 is other entry)

<221> misc\_feature  
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<223> Accession number cg41084544

<400> 2617  
tcgaactccc aacgtcaggt gatccgctg cctaggcctc ccaaagtgt g 51

<210> 2618  
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<220>  
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<221> misc\_feature  
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<223> Accession number cg41084544

<400> 2618  
tcgaactccc aacgtcaggt gatccacctg cctaggcctc ccaaagtgt g 51

<210> 2619  
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<213> Homo sapiens

<220>

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<223> 1 of 2 allelic variants (2620 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg41084998

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ggagctggga gtatccctca aagccagggc ctgggatggg cattagcttg t

51

<210> 2620

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<223> 2 of 2 allelic variants (2619 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg41084998

<400> 2620

ggagctggga gtatccctca aagccggggc ctgggatggg cattagcttg t

51

<210> 2621

<211> 51

<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> 1 of 2 allelic variants (2622 is other entry)

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg41085370

<400> 2621

aaggctctta aagcaacatt taaacttttt ggcggtgtc atttctgtga g

51

<210> 2622

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (26)...(0)

<223> 2 of 2 allelic variants (2621 is other entry)